

STIC-Biotech/ChemLib

144685

From: Bowman, Amy
Sent: Wednesday, February 09, 2005 9:04 AM
To: STIC-Biotech/ChemLib
Subject: sequence search-~~10/820,720~~ 10/820820

Please search SEQ ID NO: 4 in application 10/820,820, length limited to 150 nucleotides.

Thank you,
Amy Bowman
AU 1635

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: 2/9/05
Date Completed: 2/9/05
Searcher Prep/Rev Time: _____
Online Time: _____

Type of Search /
NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: ADT
WWW/Internet: _____
Other(Specify): _____

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 17:58:16 / Search time 1454 Seconds
(without alignments)
3165.919 Million cell updates/sec

Title: US-10-820-820-4

Sequence: 1 accguguguccguagugu.....aaacaagacagcgcuuuu 95

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 2505164

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pal:*
7: gb_pl:*
8: gb_pl:*
9: gb_pr:*
10: gb_pro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	95	E33206	
2	95	100.0	95	AX138447	E33206 Expression
3	95	100.0	95	BD015615	AX138447 Sequence
4	76.8	80.8	132	AR041184	BD015615 Slidable
5	76.8	80.8	132	AR113038	AR041184 Sequence
6	76.8	80.8	132	166463	AR113038 Sequence
7	74.8	78.7	88	BD143502	166463 Sequence 17
8	74.8	78.7	88	BD182356	BD143502 Nucleic a
9	74.8	78.7	88	AX453846	BD182356 Novel max
10	74.8	78.7	100	E47174	AX453846 Sequence
11	74.8	78.7	117	BD174675	E47174 Method for
12	74.8	78.7	137	BD143601	BD174675 Ribozyme
13	74.8	78.7	137	AX429079	BD143601 Method of
14	74.8	78.7	138	AX453858	AX429079 Sequence
15	74.8	78.7	141	AX138491	AX453858 Sequence
16	74.8	78.7	141	BD015659	AX138491 Sequence
17	74.8	78.7	142	AX138488	BD015659 Slidable
18	74.8	78.7	142	AX138489	AX138488 Sequence
19	74.8	78.7	142	AX138490	AX138489 Sequence

20	74.8	78.7	142	AX138492	AX138492 Sequence
21	74.8	78.7	142	BD015656	BD015656 Slidable
22	74.8	78.7	142	BD015657	BD015657 Slidable
23	74.8	78.7	142	BD015658	BD015658 Slidable
24	74.8	78.7	142	BD015660	BD015660 Slidable
25	74.8	78.7	128	E33205	E33205 Expression
26	74.8	78.7	136	E33203	E33203 Expression
27	74.8	78.7	142	E33204	E33204 Expression
28	74.8	78.7	75	10	K00256 Rat liver V
29	71.4	75.2	76	4	K00253 Rabbit Val-
30	71.4	75.2	76	9	K00255 Human Val-t
31	71.4	75.2	76	9	K00254 Human Val-t
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33	71.4	75.2	76	10	K00257 Rat ascites
34	71.4	75.2	149	6	E33207 Expression
35	68.2	71.8	76	10	MUSTRV1MN
36	66.8	70.3	113	6	E33209 Expression
37	66	69.5	110	6	E33208
38	65	68.4	73	5	XLTRNV
39	60.8	64.0	149	3	DROTV3BB
40	58.6	61.7	76	3	DROTV3B
41	55.4	58.3	76	3	DROTV4
42	47.4	49.9	76	8	LTRNV
43	41	43.2	76	8	YSCRV2B
44	40.4	42.5	74	8	ATTVAL
45	37.2	39.2	125	1	SMTASP

ALIGNMENTS

RESULT 1	E33206	95 bp RNA	linear	PAT 31-JAN-2002
LOCUS	E33206	Expression system for functional nucleic acid transcription.		
DEFINITION	E33206.1	GI:18624000		
VERSION	E33206	JP 2000069972-A/4.		
KEYWORDS	JP 2000069972-A/4.	synthetic construct		
SOURCE		synthetic construct		
ORGANISM		other sequences; artificial sequences.		
REFERENCE	1	(bases 1 to 95)		
AUTHORS	Tabira, K., Okawa, A. and Ozeki, S.			
TITLE	Expression system for functional nucleic acid transcription			
JOURNAL	Patent: JP 2000069972-A 4 07-MAR-2000;			
COMMENT	AGENCY OF IND SCIENCE & TECHNOL			
OS	Artificial Sequence			
PN	JP 2000069972-A/4			
PD	07-MAR-2000			
PR	31-AUG-1998	JP 1998244755		
PI	KAZUNARI TABIRA, ATSUSHI OKAWA, SHIORI OZEKI			
PC	C12N15/09, A61K31/70, A61K35/76, A61K48/00, C12N15/00	CC		
PM	Key	Location/Qualifiers		
FT	source	1. .95		
FT	source	Location/Qualifiers		
FEATURES	source	Location/Qualifiers		
ORIGIN		Location/Qualifiers		
Query Match	100.0%	Score 95; DB 6; Length 95;		
Best Local Similarity	75.8%;	Pred. No. 1.1e-21;		
Matches	72; Conservative	23; Mismatches 0; Indels 0; Gaps 0;		
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DB	1	ACCGUGUGUCCGUAGUGUACAGUGCCGUAACAGCGAAGGUGCCCGG 60		
QY	61	UUCGAAACCGGCGGAAACAAAGACAGUGCGCUUUU 95		

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	/organism="synthetic construct"					
	/mol_type="genomic RNA"					
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Best Local Similarity	75.8%;	Pred. No. 1.1e-21;	Indels 0;	Gaps 0;		
Matches	72;	Conservative 23;	Mismatches 0;			
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DB	1 ACCGTTGGTTCCGTAGTGTATGCTGTTATACGTTCCCTTAACACGCGAAAGGTCGCCGG 60					
QY	61 UUCGAAACCGGGCGGAAACAAAGCAUUCGCUUU 95					
DB	61 TTCGAAACCGGGCGGAAACAAAGCAAGTCGCTTT 95					
RESULT 4						
LOCUS	AR041184	132 bp	DNA	linear	PAT 29-SEP-1999	
DEFINITION	Sequence 17 from patent US 581275.					
ACCESSION	AR041184					
VERSION	AR041184.1	GI:5961680				
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 132)					
TITLE	Wong-Staal,F., Yu,M., Yamada,O., O'wang,J.O., Leavitt,M. and Ho,A.					
JOURNAL	HIV-specific ribozymes					
FEATURES	Patent: US 581275-A 17 22-SEP-1998;					
source	location/Qualifiers					
	1..132					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
ORIGIN						
Query Match	80.8%;	Score 76.6;	DB 6;	Length 132;		
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Matches	60;	Conservative 18;	Mismatches 2;	Indels 0;	Gaps 0;	
QY	1 ACCGUGGUVUCCGUAAGUGAGUGUUAUCACGUVUCCCUAACACGCGAAAGGUVCCCGG 60					
DB	11 ACCGTTGGTTCCGTAGTGTATGCTGTTATACGTTCCCTTAACACGCGAAAGGTCGCCGG 70					
QY	61 UUCGAAACCGGGCGGAAACA 80					
DB	71 TTCGAAACCGGGCGGAAACA 90					
RESULT 5						
LOCUS	AR113038	132 bp	DNA	linear	PAT 16-MAY-2001	
DEFINITION	Sequence 17 from patent US 6132962.					
ACCESSION	AR113038					
VERSION	AR113038.1	GI:14093360				
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 132)					
TITLE	Wong-Staal,F., Yu,M., Yamada,O., O'wang,J.O., Leavitt,M.C. and Ho,A.					
JOURNAL	Retroviral vectors comprising an anti-hiv or other nucleic acid					
FEATURES	Patent: US 6132962-A 17 17-OCT-2000;					
source	location/Qualifiers					
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/mol_type="unassigned DNA"
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Query Match	80.8%	Score 76.8;	DB 6;	Length 132;
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Matches 60;	Conservative 18;	Mismatches 2;	Indels 0;	Gaps 0;

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|||:::|||||:::|||||:::|||||:::|||||
Db 11 ACCGTTGGTTCCGTAAGTATGAGTTATCAAGTTCCGCTCACACGCGAAGCGTCCCG 70

Oy	61	UTCGAAACCGGGCGGAAACA	80
		:::	
Db	71	TTCGAACCGGGCGGAAACA	90

RESULT 6

LOCUS	166463	132 bp	DNA	linear	PAT 28-DEC-1997
DEFINITION	Sequence 17 from patent US 5670361.				

REFERENCE 1 (bases 1 to 132)
Wong-Staal, F., Yu, M., Yamada, O., Ojwang, J. O., Leavitt, M. C. and
Ho, A.,
HIV-specific ribozymes
Patent: US 5670361 A 17 23-SNP-1997;
JOURNAL Location/Qualifiers
FEATURES
source
1..132

ORIGIN

Query Match	80.8%	Score 76.8;	DB 6;	Length 132;
Best Local Similarity	75.0%	Pred. No. 1.9e-15;		
Matches 60;	Conservative 18;	Mismatches 2;	Indels 0;	Gaps 0;

DY
D6

1 ACCGTTGGAGTTCGGUAGUGUAGGAGUTUACAAGTCCGCCUAACAGCGAAAGGUCCCCGG 60
|||:::||::||::||::||::||::||::||::||::||::||::||
11 ACCGTGGTTCCTAGTAGTAGGTATCAAGTTCGCCTCACACGCGAAGCGTCCCCGG 70

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Oy      61  UTCGAACCGGGCGGGAACA  80
          ::|||||
Db      71  TTCGAACCGGGCGGGAACA  90

```

RESULT 7

LOCUS	BD143502	88 bp	RNA	linear	PAT 17-JAN-2003
DEFINITION	Nucleic acid enzyme acquiring activity of cleaving other specific target RNA by recognizing RNA molecule.				

PII KAZUNARI TAIRA, MASAKI MARASHINA, TOMOKO MARASHINA PC
C12N5/09, A61K9/127, A61K38/46, A61K46/00, A61P31/12, A61P35/00, PC
C12N1/15,
PC C12N1/19, C12N1/21, C12N5/10, C12N9/00, C12Q1/25, C12Q1/68, C12N15/
PC 00, A61K37/54,
PC C12N5/00
CC Description of Artificial Sequence: rRNAVal promoter sequence
FH Key Location/Qualifiers
FT source 1..88
FT *organism*='Artificial Sequence'.

ORIGIN

Query Match	78.7%	Score 74.8	DB 6	length 88
Best Local Similarity	70.9%	Pred. No. 9.5e-15		
Matches 61; Conservative	18	Mismatches 7	Indels 0	Gaps 0

Dy 1 ACCGTGGUUCCGUAGUGAUGGUTUAACAGUCCGCCUACAACGGAAAGUCCCCG 60
|||:::||:||||:||||:||||:||||:||||:||||:
Db 1 ACCGTGGTTCCGTAAGTAGTGTTATCACGTTCCGCTAACACGGGAAGTCCCCG 60

QY	61	UUCGAAACCGGCGGAAACAAAGACA	86
		:::	
Db	61	TTCGAAACCGGCGCACTACAAAACCA	86

RESULT 8

LOCUS	BD182356	88 bp	RNA	linear	PAT 15-MAY-2003
DEFINITION	Novel maxilzyme.				
ACCESSION	BD182356				
VERSION	BD182356.1	GI:30793274			
KEYWORDS	WO 02092821-A/3.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

COMMENT

FEATURES			
PI	TOSHIFUMI HARA, TMAO NOZAWA		NOVEL
PC	C12N15/55, C12N9/22, C12J1/34, A61K48/00, A61K38/43		CC
maxlyme			
Key	Location/Qualifiers		
PI	1. .87		
FT	/organisms='Homo sapiens (human)'. .		
FT	Location/Qualifiers		

FEATURES
SOURCE

ORIGIN

Query Match	78.7%;	Score 74.8;	DB 6;	Length 88;
Best Local Similarity	70.9%;	Pred. No. 9.5e-15;		
Matches	61;	Conservative	18;	Mismatches 7;
				Indels 0;
				Gaps 0;

Qy	1	ACCGUGUUNUCCGUAAGUGUGUUAUCGUGUCGUAAACGCGGAAAGUCCCCGG	60
Db	1	ACCGTGGTTTCCGTAAGTGTAGTGTATTCACGTTCCCTAACCGGAAAGTCCCCGG	60
Qy	61	UUCGMAACCGGCGCGAACAAGACA	86
Db	61	TTCGMAACCGGCGACTACAAAACCA	86
RESULT 9			
LOCUS	AX453846	88 bp	RNA
DEFINITION	Sequence 5 from Patent EP1213351.	linear	PAT 06-JUL-2002
ACCESSION	AX453846		
VERSION	AX453846.1	GI:21713515	
KEYWORDS	.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	other sequences; artificial sequences.		
AUTHORS	1		
TITLE	Taira,K., Warashina,M. and Warashina,T.		
JOURNAL	Nucleic acid enzymes acquiring an activity for cleaving a target rna by recognising another molecule		
FEATURES	Patent: EP 1213351-A 5 12-JUN-2002;		
source	National Institute of Advanced Industrial Science and Technology (Jp)		
ORIGIN	1..88		
Query Match	78.7%; Score 74.8; DB 6; Length 88;		
Beat Local	Similarity 70.9%; Pred. No. 9.5e-15;		
Matches	61; Conservative 18; Mismatches 7; Indels 0; Gaps 0;		
Qy	1	ACCGUGUUNUCCGUAAGUGUGUUAUCGUGUCGUAAACGCGGAAAGUCCCCGG	60
Db	1	ACCGTGGTTTCCGTAAGTGTAGTGTATTCACGTTCCCTAACCGGAAAGTCCCCGG	60
Qy	61	UUCGMAACCGGCGCGAACAAGACA	86
Db	61	TTCGMAACCGGCGACTACAAAACCA	86
RESULT 10			
LOCUS	E47174	100 bp	DNA
DEFINITION	Method for selecting active ribozyme.	linear	PAT 27-AUG-2002
ACCESSION	E47174		
VERSION	E47174.1	GI:22553362	
KEYWORDS	JP 2001128682-A/9.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 100)		
TITLE	Tabira,K. and Kawasaki,H.		
JOURNAL	Method for selecting active ribozyme		
COMMENT	Patent: JP 2001128682-A 9 15-MAY-2001;		
source	AGENCY OF IND SCIENCE & TECHNOL		
OS	Homo sapiens (human)		
PN	JP 2001128682-A/9		
PD	15-MAY-2001		
PF	05-NOV-1999	JP 1999314579	
PI	KAZUARI TABIRA,HIROAKI KAWASAKI		
PC	C12N15/09, C12Q1/68//C12N5/10, C12N5/00, C12N5/00	CC	
FEATURES	Key	Location/Qualifiers.	
source	1..100	Location/Qualifiers	

[illegible]

KEYWORDS	JP 2002125685-A/2.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1 (bases 1 to 137)
TITLE	Taira, K. and Sano, M.
JOURNAL	Method of selecting high-function nucleic acid molecule in cell
COMMENT	Patent: JP 2002125685-A 2 08-MAY-2002; DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND HIROSHI YATSUNASHI, TECHNOLOGY, KAZUNARI TAIRA OS Artificial Sequence PN JP 2002125685-A/2 PP 08-MAY-2002 JP 2000331347 PP 30-OCT-2000 JP 2000331347 PI KAZUNARI TAIRA, MASA-YUKI SANO PC C12N15/09, C12N9/00, C12Q1/02, C12Q1/25, C12Q1/68, C12N15/00 CC Description of Artificial Sequence: Sequence of rRNA-Luc GUA CC Rz
FEATURES	<p>FT Key Location/Qualifiers</p> <p>FT source 1..137</p> <p>Location/Qualifiers</p> <p>1..137</p> <p>/organism="Artificial Sequence".</p> <p>/organism="synthetic construct"</p> <p>/mol_type="genomic RNA"</p> <p>/db_xref="taxon:32630"</p>
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Matches	61; Conservative 18; Mismatches 7; Indels 0; Gaps 0;
Qy	1 ACCGUGGUGUUCGGUAGUGUAGUGUUAUCACGUCGCGCUAACACGCGAAGAGUCCCGG 60
Db	1 ACCGTTGGTTCCCGTAGTGATGTTATCACTTCGCGCTAACACGCGAAGAGTCCCGG 60
Qy	61 UUCGAAACCGGCGCGAACAACAAACA 86
Db	61 TTCGAAACCGGCGCACTACAAACAACA 86
RESULT 13	
AX429079	137 bp RNA linear PAT 21-JUN-2002
LOCUS	AX429079
DEFINITION	Sequence 2 from Patent EP1201251.
ACCESSION	AX429079
VERSION	AX429079.1 GI:21540419
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	1 synthetic construct
AUTHORS	synthetic construct
TITLE	other sequences; artificial sequences.
JOURNAL	Taira, K. and Sano, M.
FEATURES	Method for selecting highly functional nucleic acid molecules
SOURCE	within cells
Location/Qualifiers	Patent: EP 1201751-A 2 02-MAY-2002;
1	National Institute of Advanced Industrial Science and Technology
1..137	(JP)
/organism="synthetic construct"	
/mol_type="unassigned RNA"	
/db_xref="taxon:32630"	
/note="Sequence of rRNA-Luc GUA Rz"	
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Query Match	78.7%; Score 74.8; DB 6; Length 137;
Best Local Similarity	70.9%; Pred. No. 9.5e-15;
Matches	61; Conservative 18; Mismatches 7; Indels 0; Gaps 0;
Qy	1 ACCGUGGUGUUCGGUAGUGUAGUGUUAUCACGUCGCGCUAACACGCGAAGAGUCCCGG 60
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[illegible]


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/ STREET: 201 NORTH FIGUEROA STREET
/ CITY: LOS ANGELES
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 90012
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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US94/05700
/ FILING DATE: 17 MAY 1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BERLINER, ROBERT
/ REGISTRATION NUMBER: 20,121
/ REFERENCE/DOCKET NUMBER: 5555-209
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 213-977-1001
/ TELEFAX: 213-977-1003
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 133 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 97
/ OTHER INFORMATION: /note="W" = INTERNAL NUCLEOTIDE
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/ OTHER INFORMATION: SEQUENCE"
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PCT-US94-05700-17

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QY 61 UUCGAAACCGGCGGAAACAAGACAGUCGCUUU 95
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DB 71 TTCGAAACCGGCGGAAACAAGATCCWAGCGCTT 105
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RESULT 3
US-08-245-742A-17
/ Sequence 17, Application US/08245742A
/ Patent No. 5670361
/
/ GENERAL INFORMATION:
/ APPLICANT: Wong-Scaal, Flossie
/ APPLICANT: Yu, Mang
/ APPLICANT: Yamada, Oeamu
/ APPLICANT: Ojwang, Joshua O.
/ APPLICANT: Leavitt, Mark
/ APPLICANT: Ho, Anthony
/ TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
/ TITLE OF INVENTION: and AIDS
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Townsend and Townsend and Crew
/ STREET: One Market Plaza, Stewart Street Tower
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94105-1492
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US94/05700
/ FILING DATE: 17 MAY 1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BERLINER, ROBERT
/ REGISTRATION NUMBER: 20,121
/ REFERENCE/DOCKET NUMBER: 5555-209
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 213-977-1001
/ TELEFAX: 213-977-1003
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 133 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 97
/ OTHER INFORMATION: /note="W" = INTERNAL NUCLEOTIDE
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/ OTHER INFORMATION: SEQUENCE"
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PCT-US94-05700-17
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/ APPLICATION NUMBER: US/08/245,742A
/ FILING DATE: 17-MAY-1994
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/062,465
/ FILING DATE: 17-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Weber, Kenneth A.
/ REGISTRATION NUMBER: 31,677
/ REFERENCE/DOCKET NUMBER: 2307E-567-10
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 543-9600
/ TELEFAX: (415) 543-5043
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 132 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
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/ FEATURE:
/ NAME/KEY: -
/ LOCATION: (96*97)
/ OTHER INFORMATION: /note="insertion location of
/ OTHER INFORMATION: foreign gene in pol III
/ OTHER INFORMATION: transcription cassette in
/ OTHER INFORMATION: vector pMT"
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US-08-245-742A-17

Query Match      80.8%; Score 76.8; DB 1; Length 132;
Best Local Similarity 75.0%; Pred. No. 2.7e-20;
Matches 60; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGUUGUUUCGUGUGUAGUGUUAUCACGUGCCUACACCGGAAAGUCCCCCG 60
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 11 ACCGTTGGTTTCCTCGTAGTGTTATCATCGTGCCTCACACCGGAGGTCCCCCG 70
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 61 UUCGAAACCGGCGGAAACA 80
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 71 TTCGAAACCGGCGGAAACA 90
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 4
US-08-465-483-17
/ Sequence 17, Application US/08465483
/ Patent No. 5811275
/
/ GENERAL INFORMATION:
/ APPLICANT: Wong-Scaal, Flossie
/ APPLICANT: Yu, Mang
/ APPLICANT: Yamada, Oeamu
/ APPLICANT: Ojwang, Joshua O.
/ APPLICANT: Leavitt, Mark
/ APPLICANT: Ho, Anthony
/ TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
/ TITLE OF INVENTION: and AIDS
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Townsend and Townsend and Crew
/ STREET: One Market Plaza, Stewart Street Tower
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94105-1492
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/465,483
/ FILING DATE: 05-JUN-1995
/ CLASSIFICATION: 514
```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,465
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,742
FILING DATE: 17-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 2307E-567-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: (96*97) /note= "insertion location of
OTHER INFORMATION: foreign gene in pol iii
OTHER INFORMATION: transcription cassette in
OTHER INFORMATION: vector pMT"

US-08-465-483-17

Query Match 80.8%; Score 76.8; DB 1; Length 132;
Best Local Similarity 75.0%; Pred. No. 2.7e-20;
Matches 60; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGUUCGAGUGUAGUAGUUAUACAGUUGCCUACAGCGGAAGUCCCCGG 60
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 11 ACCGTGGTTCCGTAGTGTAGTGTATCACGTTGCTCTCACGCGAACGTCCTCCGG 70
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 61 UUCGAAACCGGCGGGAACA 80
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
71 TTCGAAACCGGCGGGAACA 90

RESULT 5
US-08-876-996-17
Sequence 17, Application US/08876996
Patent No. 6132962
GENERAL INFORMATION:
APPLICANT: Wong-Staal, Flossie
APPLICANT: Yu, Mang
APPLICANT: Yamada, Osamu
APPLICANT: Oiwang, Joshua O.
APPLICANT: Leavitt, Mark
APPLICANT: Ho, Anthony
TITLE OF INVENTION: Ridozyme Gene Therapy for HIV Infection
TITLE OF INVENTION: and AIDS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSES: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/876,996
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,742
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 2307E-567-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: (96*97) /note= "insertion location of
OTHER INFORMATION: foreign gene in pol iii
OTHER INFORMATION: transcription cassette in
OTHER INFORMATION: vector pMT"

US-08-876-996-17

Query Match 80.8%; Score 76.8; DB 3; Length 132;
Best Local Similarity 75.0%; Pred. No. 2.7e-20;
Matches 60; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGUUCGAGUGUAGUAGUUAUACAGUUGCCUACAGCGGAAGUCCCCGG 60
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 11 ACCGTGGTTCCGTAGTGTAGTGTATCACGTTGCTCTCACGCGGAAGUCCCCGG 70
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 61 UUCGAAACCGGCGGGAACA 80
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
71 TTCGAAACCGGCGGGAACA 90

RESULT 6
US-09-763-590-3
Sequence 3, Application US/09763590
Patent No. 6740750
GENERAL INFORMATION:
APPLICANT: TAIRA, KAZUNARI
APPLICANT: OHKAWA, JUN
APPLICANT: KOSAKI, SHIORI
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
TITLE OF INVENTION: NUCLEIC ACIDS
FILE REFERENCE: 04853.0059-00000
CURRENT APPLICATION NUMBER: US/09/763,590
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/JP99/04718
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: JP 10/244755
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 128
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: sequence of R21

US-09-763-590-3

Query Match 77.9%; Score 74; DB 4; Length 128;
Best Local Similarity 93.9%; Pred. No. 3.3e-19;
Matches 77; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCGUGUUCGAGUGUAGUAGUUAUACAGUUGCCUACAGCGGAAGUCCCCGG 60
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 1 ACCGUGUUCGAGUGUAGUAGUUAUACAGUUGCCUACAGCGGAAGUCCCCGG 60

QY 61 UUCGAAACCGGCGGAAACAA 82
DB 61 UUCGAAACCGGCGGACCCACACA 82

RESULT 7

US-09-763-590-1
Sequence 1, Application US/09763590
Patent No. 6740750
GENERAL INFORMATION:
APPLICANT: TAIRA, KAZUNARI
APPLICANT: OHKAWA, JUN
APPLICANT: KOSEKI, SHIORI
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
FILE REFERENCE: 04853.0059-00000
CURRENT APPLICATION NUMBER: US/09/763,590
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/JP99/04718
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: JP 10/244755
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 135
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
US-09-763-590-1

Query Match 76.8%; Score 73; DB 4; Length 135;
Best Local Similarity 93.8%; Pred. No. 8.1e-19;
Matches 76; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCGUGUGUUCGUGAGUGUGUACGUGUACGUGUCCUACACGCGAAAGUCCCGG 60
DB 1 ACCGUGUGUUCGUGAGUGUGUACGUGUACGUGUCCUACACGCGAAAGUCCCGG 60
QY 61 UUCGAAACCGGCGGAAACAA 81
DB 61 UUCGAAACCGGCGGACUACAA 81

RESULT 8

US-09-763-590-2
Sequence 2, Application US/09763590
Patent No. 6740750
GENERAL INFORMATION:
APPLICANT: TAIRA, KAZUNARI
APPLICANT: OHKAWA, JUN
APPLICANT: KOSEKI, SHIORI
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
FILE REFERENCE: 04853.0059-00000
CURRENT APPLICATION NUMBER: US/09/763,590
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/JP99/04718
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: JP 10/244755
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 141
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: sequence of R23

US-09-763-590-2

Query Match 76.8%; Score 73; DB 4; Length 141;
Best Local Similarity 93.8%; Pred. No. 8.3e-19;
Matches 76; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCGUGUGUUCGUGAGUGUGUACGUGUACGUGUCCUACACGCGAAAGUCCCGG 60
DB 1 ACCGUGUGUUCGUGAGUGUGUACGUGUACGUGUCCUACACGCGAAAGUCCCGG 60
QY 61 UUCGAAACCGGCGGAAACAA 81
DB 61 UUCGAAACCGGCGGACUACAA 81

RESULT 9

US-09-763-590-5
Sequence 5, Application US/09763590
Patent No. 6740750
GENERAL INFORMATION:
APPLICANT: TAIRA, KAZUNARI
APPLICANT: OHKAWA, JUN
APPLICANT: KOSEKI, SHIORI
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
FILE REFERENCE: 04853.0059-00000
CURRENT APPLICATION NUMBER: US/09/763,590
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/JP99/04718
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: JP 10/244755
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 149
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
US-09-763-590-5

Query Match 73.5%; Score 69.8; DB 4; Length 149;
Best Local Similarity 97.3%; Pred. No. 1.5e-17;
Matches 71; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGUGUUCGUGAGUGUGUACGUGUACGUGUCCUACACGCGAAAGUCCCGG 60
DB 1 ACCGUGUGUUCGUGAGUGUGUACGUGUACGUGUCCUACACGCGAAAGUCCCGG 60
QY 61 UUCGAAACCGGCG 73
DB 61 UUCGAAACCGGCG 73

RESULT 10

US-09-763-590-7/c
Sequence 7, Application US/09763590
Patent No. 6740750
GENERAL INFORMATION:
APPLICANT: TAIRA, KAZUNARI
APPLICANT: OHKAWA, JUN
APPLICANT: KOSEKI, SHIORI
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
FILE REFERENCE: 04853.0059-00000
CURRENT APPLICATION NUMBER: US/09/763,590
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/JP99/04718
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: JP 10/244755
PRIOR FILING DATE: 1998-08-31

```
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 7
/ LENGTH: 113
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Sequence of an
/ Patent No. 6740750
/ OTHER INFORMATION: antisense oligonucleotide linker
US-09-763-590-7
```

```
Query Match          70.3%; Score 66.8; DB 4; Length 113;
Best Local Similarity 71.4%; Pred. No. 2e-16;
Matches 50; Conservative 18; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 ACCGUGUUCUGUAGUGUUAUCAGUUGCCUAAACCGGAAGUCCCGG 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 71 ACCGTTGGTTTCCGTAGTGTATCATCGTTCCTAACACGCGAAGGTCCCGG 12
```

```
QY 61 UUCGAACCG 70
    ::|||
DB 11 TTCGAAGTCG 2
```

```
RESULT 11
US-09-763-590-6
/ Sequence 6, Application US/09763590
/ Patent No. 6740750
/ GENERAL INFORMATION:
```

```
/ APPLICANT: TAIIRA, KAZUNARI
/ APPLICANT: OHKAWA, JUN
/ APPLICANT: KOSEKI, SHIORI
```

```
/ TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
/ FILE REFERENCE: 04853.0059-00000
/ CURRENT APPLICATION NUMBER: US/09/763,590
```

```
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: PCT/JP99/04718
```

```
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: JP 10/244755
```

```
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 25
```

```
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 110
```

```
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
```

```
/ Patent No. 6740750
/ OTHER INFORMATION: sense oligonucleotide linker
US-09-763-590-6
```

```
Query Match          69.5%; Score 66; DB 4; Length 110;
Best Local Similarity 72.7%; Pred. No. 4.1e-16;
Matches 48; Conservative 18; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ACCGUGUUCUGUAGUGUUAUCAGUUGCCUAAACCGGAAGUCCCGG 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 44 ACCGTTGGTTTCCGTAGTGTATCATCGTTCCTAACACGCGAAGGTCCCGG 103
```

```
QY 61 UUCGAACCG 66
    ::|||
DB 104 TTCGAAC 109
```

```
RESULT 12
US-09-763-590-13/C
/ Sequence 13, Application US/09763590
/ Patent No. 6740750
/ GENERAL INFORMATION:
```

```
/ APPLICANT: TAIIRA, KAZUNARI
```

```
/ APPLICANT: OHKAWA, JUN
```

```
/ APPLICANT: KOSEKI, SHIORI
```

```
/ TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
```

```
/ FILE REFERENCE: 04853.0059-00000
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/ CURRENT APPLICATION NUMBER: US/09/763,590
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/ PRIOR FILING DATE: 2001-06-05
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/ PRIOR APPLICATION NUMBER: PCT/JP99/04718
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```
/ PRIOR FILING DATE: 1999-08-31
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```
/ PRIOR APPLICATION NUMBER: JP 10/244755
```

```
/ PRIOR FILING DATE: 1998-08-31
```

```
/ NUMBER OF SEQ ID NOS: 25
```

```
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 13
/ LENGTH: 106
```

```
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
```

```
/ Patent No. 6740750
/ OTHER INFORMATION: lower primer including the sequences of R23 and a
```

```
/ OTHER INFORMATION: terminator
US-09-763-590-13
```

```
Query Match          26.3%; Score 25; DB 4; Length 106;
Best Local Similarity 88.0%; Pred. No. 4.2;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 49 AAAGUCCCCGUGUUGCAAAACCGGCG 73
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 106 AAAGTCCCGGTTCCGAACCGGCG 82
```

```
RESULT 13
US-09-763-590-12/C
/ Sequence 12, Application US/09763590
/ Patent No. 6740750
/ GENERAL INFORMATION:
```

```
/ APPLICANT: TAIIRA, KAZUNARI
/ APPLICANT: OHKAWA, JUN
/ APPLICANT: KOSEKI, SHIORI
```

```
/ TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
```

```
/ FILE REFERENCE: 04853.0059-00000
/ CURRENT APPLICATION NUMBER: US/09/763,590
```

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/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: PCT/JP99/04718
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```
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: JP 10/244755
```

```
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 25
```

```
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 109
```

```
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
```

```
/ Patent No. 6740750
/ OTHER INFORMATION: lower primer including the sequences of R22 and a
```

```
/ OTHER INFORMATION: terminator
US-09-763-590-12
```

```
Query Match          26.3%; Score 25; DB 4; Length 109;
Best Local Similarity 88.0%; Pred. No. 4.2;
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 49 AAAGUCCCCGUGUUGCAAAACCGGCG 73
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 109 AAAGTCCCGGTTCCGAACCGGCG 85
```

```
RESULT 14
```

US-09-355-221-6/c
Sequence 6, Application US/09355221
Patent No. 6605429
GENERAL INFORMATION:
APPLICANT: Barber, Jack
APPLICANT: Welch, Peter
APPLICANT: Yel, Soomin
APPLICANT: Tritz, Richard
APPLICANT: Immunol Incorporated
TITLE OF INVENTION: Gene Functional Analysis and Discovery Using Randomized or
FILE REFERENCE: 016556-00300US
CURRENT APPLICATION NUMBER: US/09/355,221
CURRENT FILING DATE: 1999-07-23
PRIOR APPLICATION NUMBER: US 60/037,352
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: WO PCT/US98/01196
PRIOR FILING DATE: 1998-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 2.1
SEQ ID NO 6
LENGTH: 81
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: tRNA-ribozyme 11b
OTHER INFORMATION: PCR primer (tRNA-Rz 11b primer)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(81)
OTHER INFORMATION: n = g, a, c or t
US-09-355-221-6

Query Match 24.2% Score 23; DB 4; Length 81;
Best Local Similarity 91.3%; Pred. No. 23;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 58 CGGUUCGAACCGGCGGAACA 80
DB 81 CGGTCGAACCGGCGGAACA 59

RESULT 15
US-09-563-794B-71
Sequence 71, Application US/09563794B
Patent No. 6808876
GENERAL INFORMATION:
APPLICANT: KRUGER, MARTIN
APPLICANT: WELCH, PETER J.
APPLICANT: BARBER, JACK R.
TITLE OF INVENTION: CELLULAR REGULATORS OF INFECTIOUS AGENTS AND METHODS OF
FILE REFERENCE: 039316-0801
CURRENT APPLICATION NUMBER: US/09/563,794B
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 71
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: primer
US-09-563-794B-71

Query Match 23.6% Score 22.4; DB 4; Length 24;
Best Local Similarity 70.8%; Pred. No. 26;
Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 24 GGUUUCACGUGCGCTUACACGC 47
DB 1 GGTATACACGTTCCGCTCACACGC 24

Search completed: February 18, 2005, 22:34:48
Job time : 100 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 21:38:28 | Search time 253 Seconds
(without alignments)

235.207 Million cell updates/sec

Title: US-10-820-820-4

Perfect score: 95
1 accguguguuuccguagugu.....aacaagagcagcguuuu 95.

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 514866 seqs, 31196961 residues

Total number of hits satisfying chosen parameters: 10002998

Minimum DB seq length: 0
Maximum DB seq length: 150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Pending Patents_NA_New.*

1: /cgn2_6/ptodata/2/pna/PCCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq.*
8: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq.*
9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	21.8	22.9	78	US-10-932-182A-166715, Sequence 166715, A
2	18.8	19.8	77	US-10-605-923-15457, Sequence 15457, A
3	18.4	19.4	117	US-10-932-182A-174531, Sequence 174531, A
4	18.2	19.2	103	US-10-605-923-10887, Sequence 10887, A
5	18.2	19.2	103	US-10-605-924-7522, Sequence 7522, A
6	18.1	18.9	95	US-11-043-312-11, Sequence 11, Appl
7	18.1	18.9	117	US-10-707-003-1264, Sequence 1264, Ap
8	18.1	18.9	117	US-10-604-984-1264, Sequence 1264, Ap
9	18.1	18.9	100	US-10-153-469A-3, Sequence 3, Appl
10	17.6	18.5	96	US-10-932-182A-173417, Sequence 173417, A
11	17.6	18.5	104	US-10-605-923-13759, Sequence 13759, A
12	17.6	18.5	104	US-10-605-924-9585, Sequence 9585, Ap
13	17.6	18.5	112	US-11-021-016-12, Sequence 12, Appl
14	17.4	18.3	66	US-10-605-923-17798, Sequence 17798, A
15	17.4	18.3	66	US-10-605-924-12307, Sequence 12307, A
16	17.4	18.3	96	US-10-604-945-1471, Sequence 1471, Ap
17	17.4	18.3	96	US-10-604-942-65132, Sequence 65132, A
18	17.4	18.3	147	US-10-932-182A-78301, Sequence 78301, A
19	17.2	18.1	25	US-11-036-317-439867, Sequence 439867, A
20	17.2	18.1	60	US-10-708-952A-397923, Sequence 397923, A
21	17.2	18.1	65	US-10-604-945-3007, Sequence 3007, Ap
22	17.2	18.1	73	US-10-604-942-36290, Sequence 36290, A
23	17.2	18.1	73	US-10-708-952A-388244, Sequence 388244, A
24	17.2	18.1	82	US-10-604-985-809, Sequence 809, Ap

C 25	17.2	18.1	106	7	US-10-605-923-28491	Sequence 28491, A
C 26	17.2	18.1	106	7	US-10-605-924-19523	Sequence 19523, A
C 27	17.2	18.1	110	8	US-11-031-175-8522	Sequence 8522, Ap
C 28	17.2	18.1	117	6	US-10-708-952A-399286	Sequence 399286, A
C 29	17.2	18.1	144	8	US-11-043-770-4	Sequence 4, Appl
C 30	17.2	18.1	144	8	US-11-043-770-992	Sequence 992, Appl
C 31	17.2	17.9	36	5	US-09-581-528E-20	Sequence 20, Appl
C 32	17.2	17.9	60	7	US-10-605-923-6458	Sequence 6458, Ap
C 33	17.2	17.9	85	7	US-10-605-923-25873	Sequence 25873, A
C 34	17.2	17.9	90	7	US-10-605-923-3531	Sequence 3531, Ap
C 35	17.2	17.9	90	7	US-10-605-924-2441	Sequence 2441, Ap
C 36	17.2	17.9	107	7	US-10-605-923-2534	Sequence 2534, Ap
C 37	17.2	17.9	111	6	US-10-932-182A-81069	Sequence 81069, A
C 38	17.2	17.9	130	7	US-10-605-923-20831	Sequence 20831, A
C 39	17.2	17.9	130	7	US-10-605-924-14335	Sequence 14335, A
C 40	16.8	17.7	60	6	US-10-708-952A-390279	Sequence 390279, A
C 41	16.8	17.7	63	7	US-10-605-923-16921	Sequence 16921, A
C 42	16.8	17.7	63	7	US-10-605-924-11708	Sequence 11708, A
C 43	16.8	17.7	65	7	US-10-605-923-5866	Sequence 5866, Ap
C 44	16.8	17.7	65	7	US-10-605-924-4049	Sequence 4049, Ap
C 45	16.8	17.7	130	6	US-10-708-952A-396673	Sequence 396673, A

ALIGNMENTS

RESULT 1
US-10-932-182A-166715/c
Sequence 166715, Application US/10932182A
GENERAL INFORMATION:
APPLICANT: NAKAO, YOSHITIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHKARI, TOSHIHIRO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT APPLICATION NUMBER: US/10/932, 182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 166715
LENGTH: 78
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-10-932-182A-166715

Query Match 22.9%; Score 21.8; DB 6; Length 78;
Best Local Similarity 43.8%; Pred. No. 38;
Matches 32; Conservative 9; Mismatches 32; Indels 0; Gaps 0;

QY 8 GTTUCGUGUGUAGUGUUAUACAGUCGUCGCAACGGAAGGCCCCGGUGGAA 67
DB 73 GCTTCAGTACGTCACGCGCAGAGCTCAGTCTCATATCTGAAGTCCAGAGTTCGAC 14
QY 68 CCGGCGGGAACA 80
DB 13 CTCCTCGAGCA 1

RESULT 2
US-10-605-923-15457/c
Sequence 15457, Application US/10605923
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AN
FILE REFERENCE: 55000
CURRENT APPLICATION NUMBER: US/10/605, 923
CURRENT FILING DATE: 2003-11-06
NUMBER OF SEQ ID NOS: 1515668
SOFTWARE: PatentIn version 3.2
SEQ ID NO 15457

LENGTH: 77
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-605-923-15457

Query Match 19.8%; Score 18.8; DB 7; Length 77;
Best Local Similarity 45.7%; Pred. No. 5.1e+02;
Matches 21; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 16 AGUGUAGUGUUAUACAGUCCGCUAACACGCGAAGGUCGCCGU 61
DB 47 AGCGTGCATATACCTTGCTCAGACCCCAAGTCTCATGT 2

RESULT 3
US-10-932-182A-174531
Sequence 174531, Application US/10932182A

GENERAL INFORMATION:
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 174531
LENGTH: 117
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-10-932-182A-174531

Query Match 19.4%; Score 18.4; DB 6; Length 117;
Best Local Similarity 56.8%; Pred. No. 7.8e+02;
Matches 25; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

QY 30 CACGUCGCCUACACGCGAAGGUCGCCGUCGAAACCGGCG 73
DB 54 CAGGTATGCAMAGCATGCGAGAGCCCTGGGTTCATTCACAC 97

RESULT 4
US-10-605-923-10887
Sequence 10887, Application US/10605923

GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATIONALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
TITLE OF INVENTION: USBS THEROFP
FILE REFERENCE: 55000
CURRENT APPLICATION NUMBER: US/10/605,923
CURRENT FILING DATE: 2003-11-06
NUMBER OF SEQ ID NOS: 151568
SOFTWARE: Patentin version 3.2
SEQ ID NO 10887
LENGTH: 103
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-605-923-10887

Query Match 19.2%; Score 18.2; DB 7; Length 103;
Best Local Similarity 44.7%; Pred. No. 9e+02;
Matches 21; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 8 GUTUCGUGUAGUGUUAUACAGUCCGCUAACACGCGAAGGU 54
DB 21 GATTCTGACTGAATGTATGACGATATGCTTAAGCCATAGGT 67

RESULT 5
US-10-605-924-7522

Sequence 7522, Application US/10605924

GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATIONALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AN
TITLE OF INVENTION: USBS THEROFP
FILE REFERENCE: 55004
CURRENT APPLICATION NUMBER: US/10/605,924
CURRENT FILING DATE: 2003-11-06
NUMBER OF SEQ ID NOS: 138402
SOFTWARE: Patentin version 3.2
SEQ ID NO 7522
LENGTH: 103
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-605-924-7522

Query Match 19.2%; Score 18.2; DB 7; Length 103;
Best Local Similarity 44.7%; Pred. No. 9e+02;
Matches 21; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 8 GUTUCGUGUAGUGUUAUACAGUCCGCUAACACGCGAAGGU 54
DB 21 GATTCTGACTGAATGTATGACGATATGCTTAAGCCATAGGT 67

RESULT 6
US-11-043-312-11

Sequence 11, Application US/11043312

GENERAL INFORMATION:
APPLICANT: COLOSI, PETER C.
TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN
RECOMBINANT AAV VIRION PRODUCTION
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/043,312
FILING DATE: 26-Jan-2005
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/177,871
FILING DATE: 19-Jun-2002
APPLICATION NUMBER: US/08/745,957
FILING DATE: 07-Nov-1996
APPLICATION NUMBER: US 60/006,402
FILING DATE: 09-Nov-1995
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.

REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 95 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-043-312-11

Query Match 18.9%; Score 18; DB 8; Length 95;
Best Local Similarity 69.2%; Pred. No. 1.1e+03;
Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 43 CACGCGAAGGUCGCCGCUUCCGAAC 68
DB 8 CACGCGTGTAGCTCCGCGTTCCGAAC 33

RESULT 7

US-10-707-003-1264
; Sequence 1264, Application US/10707003
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55030
; CURRENT APPLICATION NUMBER: US/10707,003
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 46755
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1264
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Human enterovirus C
US-10-707-003-1264

Query Match 18.9%; Score 18; DB 6; Length 117;
Best Local Similarity 39.2%; Pred. No. 1.1e+03;
Matches 29; Conservative 10; Mismatches 35; Indels 0; Gaps 0;

QY 16 AGUGAUGUGUUAUCAGUCCGCUAAGGUCGCCGCUUCCGAACCGCGCG 75
DB 7 AGTGTATATATTAGATTTCACCCACATGTGTACTCAATCGTTTTCAGAACGAG 66

QY 76 AAACAAGACAGUC 89
DB 67 TGTATAAGATAGAC 80

RESULT 8

US-10-604-984-1264
; Sequence 1264, Application US/10604984
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55010
; CURRENT APPLICATION NUMBER: US/10604,984
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 46755
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1264
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Human enterovirus C
US-10-604-984-1264

Query Match 18.9%; Score 18; DB 7; Length 117;
Best Local Similarity 39.2%; Pred. No. 1.1e+03;
Matches 29; Conservative 10; Mismatches 35; Indels 0; Gaps 0;

QY 16 AGUGAUGUGUUAUCAGUCCGCUAAGGUCGCCGCUUCCGAACCGCGCG 75
DB 7 AGTGTATATATTAGATTTCACCCACATGTGTACTCAATCGTTTTCAGAACGAG 66

QY 76 AAACAAGACAGUC 89
DB 67 TGTATAAGATAGAC 80

RESULT 9

US-10-153-469A-3

; Sequence 3, Application US/10153469A
; GENERAL INFORMATION:
; APPLICANT: GRUSKIN, ELLIOT A.
; BROCHTER, DOUGLAS
; BROKAM, JANE
; ZHANG, GUANGHUI
; PAOLELLA, DAVID

; TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESS: DILMORTH & BARRESE
; STREET: 333 EARLE O'VINGTON BOULEVARD
; CITY: UNIONDALE
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 11553

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10153,469A
; FILING DATE: 22-May-2002
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,768
; FILING DATE: 09-Oct-1998

; ATTORNEY/AGENT INFORMATION:
; NAME: STEEN, JEFFREY S

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 228-8484
; TELEFAX: (516) 228-8516

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-153-469A-3

Query Match 18.7%; Score 17.8; DB 6; Length 100;
Best Local Similarity 72.4%; Pred. No. 1.3e+03;
Matches 21; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 45 CGCGAAGGUCGCCGCUUCCGAACCGCGGC 73
DB 48 CCCGAAGGTCCGCGTGCATAGCGCGGC 76

RESULT 10

US-10-932-182A-173417/c
; Sequence 173417, Application US/10932182A
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHKIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 173417
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-173417

Query Match 18.5%; Score 17.6; DB 6; Length 96;
Best Local Similarity 46.9%; Pred. No. 1.5e+03;
Matches 15; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 15 UAGUGUAGUGUACGACGUGCCGUAACAGC 46
DB 88 TAGTGTAGTGTATCATCATCCACCTTCCAAG 57

RESULT 11

US-10-605-923-13759/c
; Sequence 13759, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13759
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-13759

Query Match 18.5%; Score 17.6; DB 7; Length 104;
Best Local Similarity 42.2%; Pred. No. 1.5e+03;
Matches 27; Conservative 8; Mismatches 29; Indels 0; Gaps 0;

QY 20 UAGUGUAGUGUACGACGUGCCGUAACAGC 79
DB 102 TATAGTGTTCGATGCTTATGATGTGACTTGTCAATTCCTTCAATTTGATTAAT 43

QY 80 AAAG 83
DB 42 AAAG 39

RESULT 12

US-10-605-924-9585/c
; Sequence 9585, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,924
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1389402
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9585
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-924-9585

Query Match 18.5%; Score 17.6; DB 7; Length 104;
Best Local Similarity 42.2%; Pred. No. 1.5e+03;
Matches 27; Conservative 8; Mismatches 29; Indels 0; Gaps 0;

QY 20 UAGUGUAGUGUACGACGUGCCGUAACAGC 79
DB 102 TATAGTGTTCGATGCTTATGATGTGACTTGTCAATTCCTTCAATTTGATTAAT 43

QY 80 AAAG 83
DB 42 AAAG 39

RESULT 13

US-11-021-016-12

; Sequence 12, Application US/11021016

; GENERAL INFORMATION:
; APPLICANT: Thompson, James D.
; TITLE OF INVENTION: IMPROVED POLYMERASE III-BASED EXPRESSION OF THERAPEUTIC
; FILE REFERENCE: MEMB00-919-E
; CURRENT APPLICATION NUMBER: US/11/021,016
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 09/630,846
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 08/512,861
; PRIOR FILING DATE: 1995-08-07
; PRIOR APPLICATION NUMBER: 08/293,520
; PRIOR FILING DATE: 1994-08-19
; PRIOR APPLICATION NUMBER: 08/337,608
; PRIOR FILING DATE: 1994-11-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TRZ-B tRNA
US-11-021-016-12

Query Match 18.5%; Score 17.6; DB 8; Length 112;
Best Local Similarity 54.7%; Pred. No. 1.5e+03;
Matches 35; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 28 AUCAGUCUGCCUACACGCGAAGGUGCCGUGUAGAACGCGCGGAAACAAAGACAG 87
DB 28 AGCGUCUGGCGCCCAACCCAGGUGUGAUGAUGAACUCUGCCGCAUAAAAAG 87

QY 88 UCGC 91
DB 88 CCGC 91

RESULT 14

US-10-605-923-17798/c
; Sequence 17798, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17798
; LENGTH: 66
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-17798

Query Match 18.3%; Score 17.4; DB 7; Length 66;
Best Local Similarity 47.5%; Pred. No. 1.6e+03;
Matches 28; Conservative 5; Mismatches 26; Indels 0; Gaps 0;

QY 12 CCGUAGUGUAGUGUAGUACGUGCCGUAACAGC 70
DB 65 CTGACGTGAACCATCATCACCGAACCCAGAGGCGGAGAGGTCCGATGTGGAACCG 7

RESULT 15

US-10-605-924-12307/c
; Sequence 12307, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND

```

; TITLE OF INVENTION:  USES THEREOF
; FILE REFERENCE:  55004
; CURRENT APPLICATION NUMBER:  US/10/605,924
; CURRENT FILING DATE:  2003-11-06
; NUMBER OF SEQ ID NOS:  1388402
; SOFTWARE:  PatentIn version 3.2
; SEQ ID NO:  12307
; LENGTH:  66
; TYPE:  DNA
; ORGANISM:  Homo Sapiens
US-10-605-924-12307

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Query Match      18.3%; Score 17.4; DB 7; Length 66;
Best Local Similarity 47.5%; Pred. No. 1.6e+03;
Matches 28; Conservative 5; Mismatches 26; Indels 0; Gaps 0;

```

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QY      12  CCGUNAGUGUAGUGUUAUACGUCGCUAACACCGGAAAGGUCGCGGUGCGAAACCG 70
DB      65  CTGACGTGGAAACCATCATCACCAGAACCCGAGAGGCGGAGGTGGGTGATGTGGAACCG 7

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Search completed: February 18, 2005, 23:20:04
Job time : 256 secs

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OM nucleic - nucleic search, using SW model

Run on: February 18, 2005, 21:00:02 / Search time 1819 Seconds
(without alignments)
1987.963 Million cell updates/sec

Title: US-10-820-820-4

Portect score: 95
Sequence: 1 accgugugnuccguguguu.....aacaagacagcugcuuuu 95

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapect 1.0

Searched: 34239544 seqes, 19032134700 residues

Total number of hits satisfying chosen parameters: 2048674

Minimum DB seq length: 0
Maximum DB seq length: 150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_ests1:
2: gb_ests2:
3: gb_hic:
4: gb_ests3:
5: gb_ests4:
6: gb_ests5:
7: gb_ests6:
8: gb_ests1:
9: gb_ests2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	40.4	42.5	57	2	BF031637 601558122
2	31	33.6	150	5	BU275850 Cr Emb 08
3	30.2	31.8	71	9	BK203515 Danio rer
4	30	31.6	135	6	CB495943 cmykxroco
5	29.2	30.7	130	4	B1845249 f892a07.y
6	29.2	30.7	147	9	AL763279 Arabidops
7	28.2	29.7	124	9	DR3628
8	26.6	28.0	136	8	AZ927512 Danio rer
9	26.4	27.8	137	8	BZ396589 EINAN55RP
10	26.4	27.8	144	9	BK166029 Danio rer
11	26.4	27.2	149	9	DR21E13S
12	25.6	26.9	126	7	H04713
13	25.2	26.5	109	6	CD768762 AGENCOURT
14	25.2	26.5	112	6	CD768762 AGENCOURT
15	24.8	26.1	37	9	AL757571 Arabidops
16	24.8	26.1	134	9	BK126117 Danio rer
17	24.6	25.9	122	5	BQ209653 UI-R-EP0
18	24.4	25.7	121	1	AI013006 EST207457
19	24.2	25.5	64	2	BF118530 SMOVJ3CAN
20	24.2	25.5	126	2	BK247709 Danio rer
21	24	25.3	103	1	AU259857
22	24	25.3	120	9	BK233421 Danio rer
23	24	25.3	122	9	AL758258 Arabidops
24	24	25.3	123	9	BK148475 Danio rer

c	25	23.8	25.1	124	5	BW501761
c	26	23.8	25.1	128	8	BH415441 1007043B0
c	27	23.6	24.8	111	7	CK129105 AGENCOURT
c	28	23.6	24.8	112	4	B1301836
c	29	23.6	24.8	113	6	CD769729
c	30	23.6	24.8	140	5	BQ481087
c	31	23.6	24.8	143	4	B1302103
c	32	23.6	24.8	149	2	AW144501
c	33	23.6	24.8	150	7	CV252165
c	34	23.4	24.6	123	4	BM114423
c	35	23.2	24.4	106	2	AW834645
c	36	23.2	24.4	124	5	BQ342244
c	37	23.2	24.4	129	8	BZ619297
c	38	23.2	24.4	150	8	BZ619296
c	39	23	24.2	138	7	CO739722
c	40	23	24.2	143	7	CO739864
c	41	23	24.2	146	7	CO740047
c	42	23	24.2	150	7	CO739938
c	43	22.8	24.0	137	4	B1841646
c	44	22.6	23.8	73	9	AL768946
c	45	22.6	23.8	121	9	CG823338

ALIGNMENTS

RESULT 1
LOCUS BF031637
DEFINITION 601558122F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827860 5', mRNA sequence.
ACCESSION BF031637
VERSION BF031637.1 GI:10739349
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 57)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bcr-mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed By: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: L1CM497 row: 1 column: 05
High quality sequence stop: 57.
Location/Qualifiers
1..57
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3827860"
/feature="IMAGE:3827860"
/feature_type="hypertrophoma"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH MGC 58"
/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgccgcgcgcgc); Site_2: SfiI (ggcgccgcgcgcgc);
Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAAGCGCATATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCGCATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

FEATURES

source

ORIGIN

Query Match 42.5%; Score 40.4; DB 2; Length 57;
 Best Local Similarity 66.0%; Pred. No. 0.00026;
 Matches 33; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

18 UGAGUGGUAUACACGUCGCUACACGGAAGGUGCCCGGUGGAA 67
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 1 TGTAGCGTTATCATCTGCGCTCCACACGGAAGGTCCTCGGTTATTA 50

RESULT 2
 BU275850 150 bp mRNA linear EST 03-JAN-2003
 LOCUS Cr_Emb_08F08_TEXPI Convoluta roscoffensis embryos from Eva Jimenez
 DEFINITION Symagittifera roscoffensis cDNA clone Cr_Emb_08F08 5', mRNA
 sequence.

ACCESSION BU275850 GI:27476620
 VERSION BU275850
 KEYWORDS EST.
 SOURCE Symagittifera roscoffensis
 ORGANISM Symagittifera roscoffensis
 Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Acoelomorpha;
 Acoela; Sagittiferidae; Symagittifera.

REFERENCE 1 (bases 1 to 150)
 Blaxter,M.L., Jimenez,E., Rosie,A., Aboobaker,A. and Salo,E.
 A survey of genes expressed in the acoel flatworm Convoluta
 roscoffensis

JOURNAL Unpublished (2002)
 COMMENT Contact: Blaxter ML
 Institute of Cell, Animal and Population Biology
 University of Edinburgh
 Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
 3JT, UK

Tel: +44 131 650 6760
 Fax: +44 131 670 5450
 Email: mark.blaxter@ed.ac.uk
 The library was prepared by Eva Jimenez, University of Barcelona,
 Spain The sequencing was performed by Eva Jimenez, Aziz Aboobaker
 and Allie Rosie Edinburgh Phylogenomics Programme, IACPB,
 Edinburgh, UK. The sequence contained a polyA tail (trimmed)
 PCR PRIMERs
 FORWARD: 77PL
 BACKWARD: triple 5 Exseq
 Place: 08 row: F column: 08
 Seq primer: TEXPI
 High quality sequence stop: 150.
 Location/Qualifiers

FEATURES
 source
 1..150
 /organism="Symagittifera roscoffensis"
 /mol_type="mRNA"
 /db_xref="taxon:84072"
 /clone="Cr_Emb_08F08"
 /sex="mixed"
 /dev_stage="embryo"
 /clone_lib="Convoluta roscoffensis embryos from Eva
 Jimenez"

/note="Vector: lambda triplex, site_1: EcoRI; site_2:
 HindIII; The library was prepared by Eva Jimenez,
 University of Barcelona, Spain The sequencing was
 performed by Eva Jimenez, Aziz Aboobaker and Allie Rosie,
 Edinburgh Phylogenomics Programme, IACPB, Edinburgh, UK."

ORIGIN

Query Match 32.6%; Score 31; DB 5; Length 150;
 Best Local Similarity 44.8%; Pred. No. 1.1;
 Matches 39; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

7 GGUUCCGUAUGUGUACGUCGCUACACGGAAGGUGCCCGGUGGAA 66
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 26 GGAAGCAGTGCTAAGCGTTAAGCGTCCGCTCTCAATCGAAGGTCGATTCGAG 85
 67 ACCGGCGGAAACAAGACAGUCGCU 93

Db

86 GCCCACCATGATCCGCTGCTGCTGCTT 112

RESULT 3
 BX203515 71 bp DNA linear GSS 13-MAR-2003
 LOCUS Dario rerio genomic clone DKEX-224D6, genomic survey sequence.
 DEFINITION BX203515
 ACCESSION BX203515
 VERSION BX203515.1 GI:28035401
 KEYWORDS GSS.
 SOURCE Dario rerio (zebrafish)
 ORGANISM Dario rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Osteichthyes;
 Cypriniformes; Cyprinidae; Dario.

REFERENCE 1 (bases 1 to 71)
 Humphrey,S.J., Huckle,E. and Durham,J.L.
 Direct Submision
 Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome
 Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humphrey@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 224D6. 224D6 is
 part of the Dariokey BAC Library created by R. Plaetk and N.V.
 Keygene. Further details:
 http://www.sanger.ac.uk/Projects/D_rerio/
 Location/Qualifiers

FEATURES
 source
 1..71
 /organism="Dario rerio"
 /mol_type="genomic DNA"
 /db_xref="taxon:7955"
 /clone="DKEX-224D6"
 /issue_type="Testis"
 /note="Vector pindigobAC-536"

ORIGIN

Query Match 31.8%; Score 30.2; DB 9; Length 71;
 Best Local Similarity 49.3%; Pred. No. 1.9;
 Matches 33; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

9 UUUCGUAUGUAGUGUACGUCGCUACACGGAAGGUGCCCGGUGGAA 68
 ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 2 TTGAGTGGCTCAGTGTGTTAGTACGTCGCTCCACAGTAAGGTCACGTTAAATC 61

QY 69 CGGCGG 75
 DB 62 CCGGCTG 68

RESULT 4
 CB495943 135 bp mRNA linear EST 27-MAR-2003
 LOCUS omyk9c00031 Oncorhynchus mykiss Chilliack River steelhead whole
 DEFINITION Oncorhynchus mykiss cDNA, mRNA sequence.
 ACCESSION CB495943
 VERSION CB495943.1 GI:29307169
 KEYWORDS EST.
 SOURCE Oncorhynchus mykiss (rainbow trout)

ORGANISM Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 135)
 GRASP Consortium, Davidson,W.S., Koop,B.F. and
 http://web.uvic.ca/chr/grasp.

A survey of Salmo salar transcripts from high complexity cDNA
 libraries
 Unpublished (2002)
 JOURNAL Contact: Koop BF
 Centre for Biomedical Research
 University of Victoria
 PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
 Tel: 250 472 4067

/clone_11b="E1_10_12_KB"
 /note="Vector: pHO82; Site 1: BstXI; Total genomic DNA was isolated from early log phase trophozoites of E. invadens IP-1 using a Qiagen plant DNA extraction kit. A shotgun medium-size plasmid library (average insert size of 10-12 kb) was generated by random mechanical shearing of E. invadens genomic DNA, repairing the ends of DNA fragments with T4 Polymerase, adding BstXI adaptors and ligating into the BstXI site of a pUC-derived vector pHO82."

ORIGIN

Query Match 27.8%; Score 26.4; DB 8; Length 137;
 Best Local Similarity 57.7%; Pred. No. 58;
 Matches 30; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 29 UACGUGGCUAACGCGAAGGUGCCGUGGACCGGCGGAACA 80
 1 TCACATCATTTCCTACTGAGGTCGCCGGTTCAATCCGCGGAACA 52

RESULT 10
 LOCUS BX166029 144 bp DNA linear GSS 28-JAN-2003
 DEFINITION Danio rerio genomic clone DKEX-124P18, genomic survey sequence.
 ACCESSION BX166029
 VERSION BX166029.1 GI:27997576
 KEYWORDS GSS.
 SOURCE Danio rerio (zebrafish)

ORGANISM
 Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.

REFERENCE
 AUTHORS Humphray, S.J., Huckle, E. and Durham, J.L.
 TITLE Direct Substitution
 JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphray@sanger.ac.uk Unpublished

COMMENT

This sequence was generated from the T7 end of BAC 124P18. 124P18 is part of the Daniokey BAC Library created by R. Plaetzer and N.V. Keygene. Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
 Location/Qualifiers

FEATURES
 source 1..144
 /organism="Danio rerio"
 /mol_type="genomic DNA"
 /db_xref="taxon:7955"
 /clone="DKEX-124P18"
 /tissue_type="Testis"
 /note="Vector pIndigoBAC-536"

ORIGIN

Query Match 27.8%; Score 26.4; DB 9; Length 144;
 Best Local Similarity 48.5%; Pred. No. 59;
 Matches 33; Conservative 9; Mismatches 26; Indels 0; Gaps 0;

QY 12 CGUGUGUAGUGUACGUGGCUAACGCGAAGGUGCCGUGGACCGG 71
 DB 21 CAGTTGTAACGAGGAGTCAATCCCTCACGACAGAGGTCATGTTGATGATG 80

QY 72 GCGGAAC 79
 DB 81 GTTGCAGC 88

RESULT 11
 DR21E138 149 bp DNA linear GSS 27-NOV-2002
 LOCUS DR21E138
 DEFINITION Danio rerio genomic clone DKEX-21E13, genomic survey sequence.
 ACCESSION AL736659
 VERSION AL736659.1 GI:21348575
 KEYWORDS GSS.
 SOURCE Danio rerio (zebrafish)

ORGANISM

Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.

REFERENCE
 AUTHORS Humphray, S.J., Huckle, E. and Hunt, S.B.
 TITLE Direct Substitution
 JOURNAL Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humphray@sanger.ac.uk Unpublished

COMMENT

This sequence was generated from the SP6 end of BAC 21E13. 21E13 is part of the Daniokey BAC Library created by R. Plaetzer and N.V. Keygene.
 Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
 Location/Qualifiers

FEATURES

source 1..149
 /organism="Danio rerio"
 /mol_type="genomic DNA"
 /db_xref="taxon:7955"
 /clone="DKEX-21E13"
 /tissue_type="Testis"
 /note="Vector pIndigoBAC-536"

ORIGIN

Query Match 27.2%; Score 25.8; DB 9; Length 149;
 Best Local Similarity 56.6%; Pred. No. 99;
 Matches 30; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 28 AUCAGUGGCUAACGCGAAGGUGCCGUGGACCGGCGGAACA 80
 DB 4 ATCAGATCATTTCCTACTGAGGTCGCCGGTTCAATCCGCGGAACA 56

RESULT 12

LOCUS H04713 126 bp mRNA linear EST 20-JUN-1995
 DEFINITION e17-1.3.3-3' lambda Zap Express library of P. B. Schwartz (9/93)
 ACCESSION H04713
 VERSION H04713.1 GI:867646

KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE
 AUTHORS Schwartz, P.B., Grieshaber, N.A., Grieshaber, S.S. and Majack, R.A.
 TITLE An expressed sequence tag from in vitro embryonic rat vascular smooth muscle cells
 JOURNAL Unpublished (1995)

COMMENT

Contact: Phillip B. Schwartz
 Pediatric and Cellular and Structural Biology
 University of Colorado Health Sciences Center
 4200 East Ninth Avenue, Denver, Colorado, 80262, USA
 Tel: (303) 270-4569
 Fax: (303) 270-8353
 Email: schwaartz@pediatrics.hsc.colorado.edu.
 Location/Qualifiers

FEATURES

source 1..126
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="e17-1.3.3"
 /clone_11b="Lambda Zap Express library of P. B. Schwartz (9/93)"
 /note="developmental-stage=Embryonic Day 17
 post-fertilization; tissue-type=Aorta; cell-type=Vascular
 smooth muscle cell; sex=Male."

ORIGIN

Query Match 26.9%; Score 25.6; DB 7; Length 126;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 22:02:48 ; Search time 313 Seconds
(without alignments)
1793.921 Million cell updates/sec

Title: US-10-820-820-4

Perfect score: 95
1 accguguguuucguguguu.....aaacaagacagucuuuu 95

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 5307602

Minimum DB seq length: 0
Maximum DB seq length: 150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09A_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	95	US-10-361-028-8	Sequence 8, Appli
2	95	100.0	95	US-10-820-820-4	Sequence 4, Appli
3	74.8	78.7	88	US-09-974-974-5	Sequence 5, Appli
4	74.8	78.7	88	US-09-974-851A-3	Sequence 3, Appli
5	74.8	78.7	138	US-10-361-028-52	Sequence 17, Appli
6	74.8	78.7	141	US-10-361-028-49	Sequence 52, Appli
7	74.8	78.7	142	US-10-361-028-50	Sequence 50, Appli
8	74.8	78.7	142	US-10-361-028-51	Sequence 51, Appli
9	74.8	78.7	142	US-10-361-028-53	Sequence 53, Appli
10	74.8	78.7	142	US-10-820-820-3	Sequence 3, Appli
11	74	77.9	128	US-10-820-820-3	Sequence 3, Appli

12	73	76.8	135	US-10-820-820-1	Sequence 1, Appli
13	73	76.8	141	US-10-820-820-2	Sequence 2, Appli
14	69.8	73.5	149	US-10-820-820-5	Sequence 5, Appli
15	66.8	70.3	113	US-10-820-820-7	Sequence 7, Appli
16	66	69.5	110	US-10-820-820-6	Sequence 6, Appli
17	63	66.3	64	US-10-738-642-57	Sequence 57, Appli
18	35.2	37.1	73	US-10-857-625-384	Sequence 384, App
19	35.2	37.1	73	US-10-857-625-404	Sequence 404, App
20	35.2	37.1	73	US-10-857-625-407	Sequence 407, App
21	27	28.4	130	US-10-807-755-35	Sequence 35, Appli
22	27	28.4	135	US-10-807-755-25	Sequence 25, Appli
23	26	27.4	72	US-10-067-956-3	Sequence 3, Appli
24	26	27.4	72	US-10-067-956-4	Sequence 4, Appli
25	26	27.4	72	US-10-898-106-3	Sequence 3, Appli
26	26	27.4	72	US-10-898-106-4	Sequence 4, Appli
27	26	27.4	74	US-10-057-783A-30	Sequence 30, Appli
28	26	27.4	76	US-10-057-783A-27	Sequence 27, Appli
29	26	27.4	135	US-10-807-755-27	Sequence 27, Appli
30	25.8	27.2	123	US-10-083-357-557	Sequence 557, App
31	25.4	26.7	132	US-10-083-357-448	Sequence 348, App
32	25.2	26.5	64	US-09-974-300-8411	Sequence 8411, Ap
33	25.2	26.5	64	US-09-974-300-8428	Sequence 8428, Ap
34	25.2	26.5	64	US-09-974-300-8437	Sequence 8437, Ap
35	25	26.3	77	US-09-974-300-4366	Sequence 4366, Ap
36	25	26.3	77	US-09-974-300-4385	Sequence 4385, Ap
37	25	26.3	77	US-09-974-300-4400	Sequence 4400, Ap
38	25	26.3	77	US-09-974-300-4442	Sequence 4442, Ap
39	25	26.3	77	US-09-974-300-8401	Sequence 8401, Ap
40	25	26.3	77	US-09-974-300-8420	Sequence 8420, Ap
41	25	26.3	77	US-09-974-300-8435	Sequence 8435, Ap
42	25	26.3	77	US-09-974-300-8475	Sequence 8475, Ap
43	25	26.3	109	US-10-820-820-13	Sequence 13, Appli
44	25	26.3	106	US-10-820-820-12	Sequence 12, Appli
45	24.4	25.7	135	US-10-282-122A-27179	Sequence 27179, A

ALIGNMENTS

RESULT 1
US-10-361-028-8
; Sequence 8, Application US/10361028
; Publication No. US20030199471A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: MARASHINA, MASAKI
; APPLICANT: KUMABARA, TOMOKO
; APPLICANT: KAWASAKI, HIROAKI
; TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
; FILE REFERENCE: 081356/0151
; CURRENT APPLICATION NUMBER: US/10/361,028
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US/09/704,525
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: JP 316133/1999
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 95
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
; OTHER INFORMATION: Sequence of the transcript of the human placental crRNAval
US-10-361-028-8

Query Match 100.0%; Score 95; DB 16; Length 95;
Best Local Similarity 100.0%; Pred. No. 4.7e-26;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ACCGUGUUCGUGUGUGUGUACAGCGUCCGUAACGCGAAGGUCGCCGG 60
|||||

Db 1 ACCGUGUUVCCGUGAGUGUUAUACAGUCGCUAACAGCGGAAGUCCCCGG 60
QY 61 UUCGAAACCGGGCGGAAACAAAGACAGUCGCUUU 95
Db 61 UUCGAAACCGGGCGGAAACAAAGACAGUCGCUUU 95

RESULT 2

US-10-820-820-4
Sequence 4, Application US/10820820
Publication No. US20040198689A1
GENERAL INFORMATION:
APPLICANT: TAIRA, KAZUNARI
APPLICANT: OKAWA, JUN
APPLICANT: KOSBEKI, SHIORI
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
TITLE OF INVENTION: NUCLEIC ACIDS
FILE REFERENCE: 04853.0059-00000
CURRENT FILING DATE: 2004-04-09
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US/09/763,590
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/JP99/04718
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: JP 10/244755
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 95
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
US-10-820-820-4

Handwritten signature

Query Match 100.0%; Score 95; DB 18; Length 95;
Best Local Similarity 100.0%; Pred. No. 4,7e-26;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGUGUUVCCGUGAGUGUUAUACAGUCGCUAACAGCGGAAGUCCCCGG 60
Db 1 ACCGUGUUVCCGUGAGUGUUAUACAGUCGCUAACAGCGGAAGUCCCCGG 60
QY 61 UUCGAAACCGGGCGGAAACAAAGACAGUCGCUUU 95
Db 61 UUCGAAACCGGGCGGAAACAAAGACAGUCGCUUU 95

RESULT 3

US-09-974-974-5
Sequence 5, Application US/09974974
Publication No. US20030013095A1
GENERAL INFORMATION:
APPLICANT: Kazunari TAIRA
APPLICANT: Masashi WARASHINA
APPLICANT: Tomoko WARASHINA
TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
TITLE OF INVENTION: target RNA by recognizing another molecule
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/974,974
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: JP 2000-313320
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 88
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: tRNAVal promoter sequence

US-09-974-974-5

Query Match 78.7%; Score 74.8; DB 10; Length 88;
Best Local Similarity 91.9%; Pred. No. 2.3e-18;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ACCGUGUUVCCGUGAGUGUUAUACAGUCGCUAACAGCGGAAGUCCCCGG 60
Db 1 ACCGUGUUVCCGUGAGUGUUAUACAGUCGCUAACAGCGGAAGUCCCCGG 60
QY 61 UUCGAAACCGGGCGGAAACAAAGACA 86
Db 61 UUCGAAACCGGGCGGAAACAAAGACA 86

RESULT 4

US-10-475-851A-3
Sequence 3, Application US/10475851A
Publication No. US20040248114A1
GENERAL INFORMATION:
APPLICANT: TAIRA, Kazunari
APPLICANT: WARASHINA, Tomoko
APPLICANT: WARASHINA, Masaki
APPLICANT: KAWASAKI, Hiroaki
APPLICANT: HARA, Toshifumi
APPLICANT: NOZAWA, Iwao
TITLE OF INVENTION: Novel Maxizyme
FILE REFERENCE: P24426
CURRENT APPLICATION NUMBER: US/10/475,851A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/JP02/04322
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 88
TYPE: RNA
ORGANISM: Homo sapiens
US-10-475-851A-3

Query Match 78.7%; Score 74.8; DB 18; Length 88;
Best Local Similarity 91.9%; Pred. No. 2.3e-18;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ACCGUGUUVCCGUGAGUGUUAUACAGUCGCUAACAGCGGAAGUCCCCGG 60
Db 1 ACCGUGUUVCCGUGAGUGUUAUACAGUCGCUAACAGCGGAAGUCCCCGG 60
QY 61 UUCGAAACCGGGCGGAAACAAAGACA 86
Db 61 UUCGAAACCGGGCGGAAACAAAGACA 86

RESULT 5

US-09-974-974-17
Sequence 17, Application US/09974974
Publication No. US20030013095A1
GENERAL INFORMATION:
APPLICANT: Kazunari TAIRA
APPLICANT: Masashi WARASHINA
APPLICANT: Tomoko WARASHINA
TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
TITLE OF INVENTION: target RNA by recognizing another molecule
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/974,974
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: JP 2000-313320
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 138
TYPE: RNA

```
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: tRNAVal T-MzL
US-09-974-974-17

Query Match      78.7%; Score 74.8; DB 10; Length 138;
Best Local Similarity 91.9%; Pred. No. 2.5e-18;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 ACCGUGUGUUCGUGAGUGUUAUCAGGUGCCUAAACGCGAAAGGUGCCCGG 60
      1 ACCGUGUGUUCGUGAGUGUUAUCAGGUGCCUAAACGCGAAAGGUGCCCGG 60
DB      1 ACCGUGUGUUCGUGAGUGUUAUCAGGUGCCUAAACGCGAAAGGUGCCCGG 60

QY      61 UUCGAAACCGGGCGGAAACAAAGACA 86
      61 UUCGAAACCGGGCGGAAACAAAGACA 86
DB      61 UUCGAAACCGGGCGGAAACAAAGACA 86

RESULT 6
US-10-361-028-52
/ Sequence 52, Application US/10361028
/ Publication No. US20030199471A1
/ GENERAL INFORMATION:
/ APPLICANT: TAIRA, KAZUNARI
/ APPLICANT: MARASHINA, MASAKI
/ APPLICANT: KUMABARA, TOMOKO
/ APPLICANT: KAWASAKI, HIROAKI
/ TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
/ FILE REFERENCE: 081356/0151
/ CURRENT APPLICATION NUMBER: US/10/361,028
/ CURRENT FILING DATE: 2003-02-10
/ PRIOR APPLICATION NUMBER: US/09/704,525
/ PRIOR FILING DATE: 2000-11-03
/ PRIOR APPLICATION NUMBER: JP 316133/1999
/ PRIOR FILING DATE: 1999-11-05
/ NUMBER OF SEQ ID NOS: 56
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 52
/ LENGTH: 141
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
US-10-361-028-52

Query Match      78.7%; Score 74.8; DB 16; Length 141;
Best Local Similarity 91.9%; Pred. No. 2.5e-18;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 ACCGUGUGUUCGUGAGUGUUAUCAGGUGCCUAAACGCGAAAGGUGCCCGG 60
      1 ACCGUGUGUUCGUGAGUGUUAUCAGGUGCCUAAACGCGAAAGGUGCCCGG 60
DB      1 ACCGUGUGUUCGUGAGUGUUAUCAGGUGCCUAAACGCGAAAGGUGCCCGG 60

QY      61 UUCGAAACCGGGCGGAAACAAAGACA 86
      61 UUCGAAACCGGGCGGAAACAAAGACA 86
DB      61 UUCGAAACCGGGCGGAAACAAAGACA 86

RESULT 7
US-10-361-028-49
/ Sequence 49, Application US/10361028
/ Publication No. US20030199471A1
/ GENERAL INFORMATION:
/ APPLICANT: TAIRA, KAZUNARI
/ APPLICANT: MARASHINA, MASAKI
/ APPLICANT: KUMABARA, TOMOKO
/ APPLICANT: KAWASAKI, HIROAKI
/ TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
/ FILE REFERENCE: 081356/0151
/ CURRENT APPLICATION NUMBER: US/10/361,028
/ CURRENT FILING DATE: 2003-02-10
/ PRIOR APPLICATION NUMBER: US/09/704,525
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/ PRIOR FILING DATE: 2000-11-03
/ PRIOR APPLICATION NUMBER: JP 316133/1999
/ PRIOR FILING DATE: 1999-11-05
/ NUMBER OF SEQ ID NOS: 56
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 49
/ LENGTH: 142
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
US-10-361-028-49

Query Match      78.7%; Score 74.8; DB 16; Length 142;
Best Local Similarity 91.9%; Pred. No. 2.5e-18;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 ACCGUGUGUUCGUGAGUGUUAUCAGGUGCCUAAACGCGAAAGGUGCCCGG 60
      1 ACCGUGUGUUCGUGAGUGUUAUCAGGUGCCUAAACGCGAAAGGUGCCCGG 60
DB      1 ACCGUGUGUUCGUGAGUGUUAUCAGGUGCCUAAACGCGAAAGGUGCCCGG 60

QY      61 UUCGAAACCGGGCGGAAACAAAGACA 86
      61 UUCGAAACCGGGCGGAAACAAAGACA 86
DB      61 UUCGAAACCGGGCGGAAACAAAGACA 86

RESULT 8
US-10-361-028-50
/ Sequence 50, Application US/10361028
/ Publication No. US20030199471A1
/ GENERAL INFORMATION:
/ APPLICANT: TAIRA, KAZUNARI
/ APPLICANT: MARASHINA, MASAKI
/ APPLICANT: KUMABARA, TOMOKO
/ APPLICANT: KAWASAKI, HIROAKI
/ TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
/ FILE REFERENCE: 081356/0151
/ CURRENT APPLICATION NUMBER: US/10/361,028
/ CURRENT FILING DATE: 2003-02-10
/ PRIOR APPLICATION NUMBER: US/09/704,525
/ PRIOR FILING DATE: 2000-11-03
/ PRIOR APPLICATION NUMBER: JP 316133/1999
/ PRIOR FILING DATE: 1999-11-05
/ NUMBER OF SEQ ID NOS: 56
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 50
/ LENGTH: 142
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
US-10-361-028-50

Query Match      78.7%; Score 74.8; DB 16; Length 142;
Best Local Similarity 91.9%; Pred. No. 2.5e-18;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 ACCGUGUGUUCGUGAGUGUUAUCAGGUGCCUAAACGCGAAAGGUGCCCGG 60
      1 ACCGUGUGUUCGUGAGUGUUAUCAGGUGCCUAAACGCGAAAGGUGCCCGG 60
DB      1 ACCGUGUGUUCGUGAGUGUUAUCAGGUGCCUAAACGCGAAAGGUGCCCGG 60

QY      61 UUCGAAACCGGGCGGAAACAAAGACA 86
      61 UUCGAAACCGGGCGGAAACAAAGACA 86
DB      61 UUCGAAACCGGGCGGAAACAAAGACA 86

RESULT 9
US-10-361-028-51
/ Sequence 51, Application US/10361028
/ Publication No. US20030199471A1
/ GENERAL INFORMATION:
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APPLICANT: TAIRA, KAZUNARI
APPLICANT: MARASHINA, MASAKI
APPLICANT: KUMABARA, TOMOKO
APPLICANT: KAWASAKI, HIROAKI
TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
FILE REFERENCE: 081356/0151
CURRENT APPLICATION NUMBER: US/10/361,028
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US/09/704,525
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: JP 316133/1999
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 51
LENGTH: 142
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
US-10-361-028-51
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```
Query Match      78.7%; Score 74.8; DB 16; Length 142;
Best Local Similarity 91.9%; Pred. No. 2.5e-18;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 1 ACCGUGGUGUUGCGUAGUGUAGUGUUAUCACGUGCCUAAACGCGAAAGGUGCCCGG 60
DB 1 ACCGUGGUGUUGCGUAGUGUAGUGUUAUCACGUGCCUAAACGCGAAAGGUGCCCGG 60
QY 61 UUCGAAACCGGCGGCAACAAACCA 86
DB 61 UUCGAAACCGGCGGCAACAAACCA 86
```

```
RESULT 10
US-10-361-028-53
Sequence 53, Application US/10361028
Publication No. US20030199471A1
GENERAL INFORMATION:
APPLICANT: TAIRA, KAZUNARI
APPLICANT: MARASHINA, MASAKI
APPLICANT: KUMABARA, TOMOKO
APPLICANT: KAWASAKI, HIROAKI
TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
FILE REFERENCE: 081356/0151
CURRENT APPLICATION NUMBER: US/10/361,028
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US/09/704,525
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: JP 316133/1999
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 53
LENGTH: 142
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
US-10-361-028-53
```

```
Query Match      78.7%; Score 74.8; DB 16; Length 142;
Best Local Similarity 91.9%; Pred. No. 2.5e-18;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 1 ACCGUGGUGUUGCGUAGUGUAGUGUUAUCACGUGCCUAAACGCGAAAGGUGCCCGG 60
DB 1 ACCGUGGUGUUGCGUAGUGUAGUGUUAUCACGUGCCUAAACGCGAAAGGUGCCCGG 60
QY 61 UUCGAAACCGGCGGCAACAAACCA 86
```

```
DB 61 UUCGAAACCGGCGGCAACAAACCA 86
```

```
RESULT 11
US-10-820-820-3
Sequence 3, Application US/10820820
Publication No. US20040198689A1
GENERAL INFORMATION:
APPLICANT: TAIRA, KAZUNARI
APPLICANT: OKAWA, JUN
APPLICANT: KOSERI, SHIORI
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
FILE REFERENCE: 04853.0059-00000
CURRENT APPLICATION NUMBER: US/10/820,820
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: US/09/763,590
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: PCT/JP99/04718
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: JP 10/244755
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 128
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
US-10-820-820-3
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```
Query Match      77.9%; Score 74; DB 18; Length 128;
Best Local Similarity 93.9%; Pred. No. 4.9e-18;
Matches 77; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 ACCGUGGUGUUGCGUAGUGUAGUGUUAUCACGUGCCUAAACGCGAAAGGUGCCCGG 60
DB 1 ACCGUGGUGUUGCGUAGUGUAGUGUUAUCACGUGCCUAAACGCGAAAGGUGCCCGG 60
QY 61 UUCGAAACCGGCGGCAACAAACCA 82
DB 61 UUCGAAACCGGCGGCAACCAACCA 82
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```
RESULT 12
US-10-820-820-1
Sequence 1, Application US/10820820
Publication No. US20040198689A1
GENERAL INFORMATION:
APPLICANT: TAIRA, KAZUNARI
APPLICANT: OKAWA, JUN
APPLICANT: KOSERI, SHIORI
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
FILE REFERENCE: 04853.0059-00000
CURRENT APPLICATION NUMBER: US/10/820,820
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: US/09/763,590
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: PCT/JP99/04718
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: JP 10/244755
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 135
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
```

OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: Sequence of R22
US-10-820-820-1

Query Match 76.8%; Score 73; DB 18; Length 135;
Best Local Similarity 93.8%; Pred. No. 1.2e-17;
Matches 76; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCGUGUUCGAGUGUAGUGUACAGGUGCCUACACGCGAAAGGUCGCCG 60
DB 1 ACCGUGUUCGAGUGUAGUGUACAGGUGCCUACACGCGAAAGGUCGCCG 60

QY 61 UUCGAAACCGGCGGACAA 81
DB 61 UUCGAAACCGGCGGACUACAA 81

RESULT 13

US-10-820-820-2
Sequence 2, Application US/10820820
Publication No. US20040198689A1

GENERAL INFORMATION:

APPLICANT: TAIRA, KAZUNARI

APPLICANT: OHKAWA, JUN

APPLICANT: KOSAKI, SHIORI

TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL

FILE REFERENCE: 04853.0059-00000

CURRENT APPLICATION NUMBER: US/10/820,820

CURRENT FILING DATE: 2004-04-09

PRIOR APPLICATION NUMBER: US/09/763,590

PRIOR FILING DATE: 2001-02-26

PRIOR APPLICATION NUMBER: PCT/JP99/04718

PRIOR FILING DATE: 1998-08-31

PRIOR APPLICATION NUMBER: JP 10/244755

PRIOR FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 2

LENGTH: 141

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

US-10-820-820-2

Query Match 76.8%; Score 73; DB 18; Length 141;
Best Local Similarity 93.8%; Pred. No. 1.2e-17;
Matches 76; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCGUGUUCGAGUGUAGUGUACAGGUGCCUACACGCGAAAGGUCGCCG 60
DB 1 ACCGUGUUCGAGUGUAGUGUACAGGUGCCUACACGCGAAAGGUCGCCG 60

QY 61 UUCGAAACCGGCGGACAA 81
DB 61 UUCGAAACCGGCGGACUACAA 81

RESULT 14

US-10-820-820-5
Sequence 5, Application US/10820820
Publication No. US20040198689A1

GENERAL INFORMATION:

APPLICANT: TAIRA, KAZUNARI

APPLICANT: OHKAWA, JUN

APPLICANT: KOSAKI, SHIORI

TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL

FILE REFERENCE: 04853.0059-00000

CURRENT APPLICATION NUMBER: US/10/820,820

CURRENT FILING DATE: 2004-04-09

PRIOR APPLICATION NUMBER: US/09/763,590

PRIOR FILING DATE: 2001-02-26

PRIOR APPLICATION NUMBER: PCT/JP99/04718

PRIOR FILING DATE: 1998-08-31

PRIOR APPLICATION NUMBER: JP 10/244755

PRIOR FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 5

LENGTH: 149

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

US-10-820-820-5

Query Match 73.5%; Score 69.8; DB 18; Length 149;
Best Local Similarity 97.3%; Pred. No. 2e-16;
Matches 71; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGUUCGAGUGUAGUGUACAGGUGCCUACACGCGAAAGGUCGCCG 60
DB 1 ACCGUGUUCGAGUGUAGUGUACAGGUGCCUACACGCGAAAGGUCGCCG 60

QY 61 UUCGAAACCGGCGG 73
DB 61 UUCGAAACCGGCGG 73

RESULT 15

US-10-820-820-7/c

Sequence 7, Application US/10820820

Publication No. US20040198689A1

GENERAL INFORMATION:

APPLICANT: TAIRA, KAZUNARI

APPLICANT: OHKAWA, JUN

APPLICANT: KOSAKI, SHIORI

TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL

FILE REFERENCE: 04853.0059-00000

CURRENT APPLICATION NUMBER: US/10/820,820

CURRENT FILING DATE: 2004-04-09

PRIOR APPLICATION NUMBER: US/09/763,590

PRIOR FILING DATE: 2001-02-26

PRIOR APPLICATION NUMBER: PCT/JP99/04718

PRIOR FILING DATE: 1998-08-31

PRIOR APPLICATION NUMBER: JP 10/244755

PRIOR FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 7

LENGTH: 113

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Sequence of an

US-10-820-820-7

Query Match 70.3%; Score 66.8; DB 18; Length 113;
Best Local Similarity 71.4%; Pred. No. 2.6e-15;
Matches 50; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGUGUUCGAGUGUAGUGUACAGGUGCCUACACGCGAAAGGUCGCCG 60
DB 71 ACCGUGUUCGAGUGUAGUGUACAGGUGCCUACACGCGAAAGGUCGCCG 12

QY 61 UUCGAAACCGG 70
DB 11 UUCGAAACCGG 2

Tue Feb 22 13:22:42 2005

us-10-820-820-4.rnpb

Page 6

Search completed: February 18, 2005, 23:26:29
Job time : 314 secs

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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 21:34:12 ; Search time 2446 Seconds

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Title: US-10-820-820-4

Perfect score: 95

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	95	32	US-09-704-525-8
2	95	100.0	95	32	US-09-718-098-15
3	95	100.0	95	53	US-10-361-028-8
4	95	100.0	95	63	US-10-820-820-4
5	74.8	78.7	88	28	US-09-623-932-3
6	74.8	78.7	88	28	US-09-623-932A-3
7	74.8	78.7	88	44	US-09-974-974-5
8	74.8	78.7	88	55	US-10-475-851A-3
9	74.8	78.7	88	56	US-10-512-386-1
10	74.8	78.7	91	32	US-09-718-098-16
11	74.8	78.7	128	28	US-09-623-932A-20
12	74.8	78.7	135	28	US-09-623-932A-18
13	74.8	78.7	137	45	US-09-984-198A-2
14	74.8	78.7	138	44	US-09-974-974-17
15	74.8	78.7	141	32	US-09-704-525-52
16	74.8	78.7	141	53	US-10-361-028-52
17	74.8	78.7	142	32	US-09-704-525-49
18	74.8	78.7	142	32	US-09-704-525-50
19	74.8	78.7	142	32	US-09-704-525-51
20	74.8	78.7	142	32	US-09-704-525-53
21	74.8	78.7	142	53	US-10-361-028-49
22	74.8	78.7	142	53	US-10-361-028-50
23	74.8	78.7	142	53	US-10-361-028-51
24	74.8	78.7	142	53	US-10-361-028-53
25	74.8	78.7	142	53	US-10-820-820-3
26	74.8	78.7	142	53	US-10-820-820-1
27	74.8	78.7	142	53	US-10-820-820-2
28	74.8	78.7	142	53	US-10-820-820-5
29	69.8	70.3	113	63	US-10-820-820-7
30	66.8	69.5	110	63	US-10-820-820-6
31	63	66.3	64	2	PCT-US03-40292-57
32	61.8	65.1	69	16	US-09-047-925-3336
33	61.8	65.1	69	16	US-09-047-925-3336
34	61.8	65.1	69	25	US-09-540-765-43340
35	41	43.2	73	114	US-60-445-574-118
36	40	42.1	73	79	US-60-615-573-3
37	38.8	40.8	129	22	US-09-450-969-3090
38	38.8	40.8	129	62	US-10-724-972A-3090
39	38.4	40.4	73	79	US-60-615-573-10841
40	38.4	40.4	138	22	US-09-450-969-2465
41	38.4	40.4	138	62	US-10-724-972A-2465
42	35.2	37.1	73	64	US-10-857-625-384
43	35.2	37.1	73	64	US-10-857-625-404
44	35.2	37.1	73	64	US-10-857-625-407
45	35.2	37.1	73	64	US-10-859-198-3224

ALIGNMENTS

RESULT 1
US-09-704-525-8
Sequence 8, Appl1
GENERAL INFORMATION:
APPLICANT: TAIRA, KAZUNARI
APPLICANT: WAKASHINA, MASAKI
APPLICANT: KUMABARA, TOMOKO
APPLICANT: KAWASAKI, HIROAKI
TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
FILE REFERENCE: 08156/0151
CURRENT APPLICATION NUMBER: US/09/704,525
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: JP 316133/1999
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 95
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: the nucleotide sequence of the transcript of the human placental CRNAval
US-09-704-525-8

Query Match 100.0% Score 95; DB 32; Length 95;
Best Local Similarity 100.0%; Pred. No. 4e-25; 0; Indels 0; Gaps 0;
Matches 95; Conservative 0; Mismatches 0

QY 1 ACCGUGUUCUGUAGUGUUAUACAGUUGCCUAAACGCGAAAGUCCCGG 60
1 ACCGUGUUCUGUAGUGUUAUACAGUUGCCUAAACGCGAAAGUCCCGG 60
DB 61 UUCGAAACCGGCGGAAACAAAGACAGUGCCUUU 95
61 UUCGAAACCGGCGGAAACAAAGACAGUGCCUUU 95

RESULT 2
US-09-718-098-15
Sequence 15, Application US/09718098
GENERAL INFORMATION:
APPLICANT: TANAKA, MANAMI
TITLE OF INVENTION: RIBOZYMES TARGETING BRADEION TRANSCRIPTS AND USE
FILE REFERENCE: 08156/0155
CURRENT APPLICATION NUMBER: US/09/718,098
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 95
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: tRNA(Val) promoter
US-09-718-098-15

Query Match 100.0% Score 95; DB 32; Length 95;
Best Local Similarity 100.0%; Pred. No. 4e-25; 0; Indels 0; Gaps 0;
Matches 95; Conservative 0; Mismatches 0

QY 1 ACCGUGUUCUGUAGUGUUAUACAGUUGCCUAAACGCGAAAGUCCCGG 60
1 ACCGUGUUCUGUAGUGUUAUACAGUUGCCUAAACGCGAAAGUCCCGG 60
DB 1 ACCGUGUUCUGUAGUGUUAUACAGUUGCCUAAACGCGAAAGUCCCGG 60
61 UUCGAAACCGGCGGAAACAAAGACAGUGCCUUU 95
61 UUCGAAACCGGCGGAAACAAAGACAGUGCCUUU 95
DB 61 UUCGAAACCGGCGGAAACAAAGACAGUGCCUUU 95

RESULT 3
US-10-361-028-8

```

Sequence 8 Application US/10361028
GENERAL INFORMATION:
APPLICANT: TAIIRA, KAZUNARI
APPLICANT: WAKASHINA, MASAKI
APPLICANT: KUMABARA, TOMOKO
APPLICANT: KOMASAKI, HIROAKI
TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
FILE REFERENCE: 081356/0151
CURRENT APPLICATION NUMBER: US/10/361,028
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US/09/704,525
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: JP 316133/1999
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 95
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
US-10-361-028-8
sequence of the transcript of the human placental tRNAVal

```

	Query Match	Similarity	Score	DB	Length
Best Local	100.0%	100.0%	95	53	95
Matches	95	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0
QY	1	ACCGTUGGUTUCCGUAAGUAGUGUTUVCACGTCGCGCUAACAGCGCAAGATCCCGCG	60		
Db	1	ACCGUGGUTUCCGUAAGUGAGUGUUAACAGTUCGCGCUAACAGCGCAAGATGCCCCG	60		
QY	61	UUCGAAACCGGAGCGGAACAAAGACAGTGCCTUUU	95		
Db	61	UUCGAAACCGGAGCGGAACAAAGACAGTGCCTUUU	95		

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RESULT 4
US-10-820-820-4
Sequence 4, Application US/10820820
GENERAL INFORMATION:
APPLICANT: TAIRA, KAZUNARI
APPLICANT: OHKAWA, JUN
APPLICANT: KOSEKI, SHIORI
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
FILE REFERENCE: 04853.0059-00000
CURRENT APPLICATION NUMBER: US/10/820, 820
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: US/09/763, 590
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: PCT/JP99/04718
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: JP 10/244755
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 95
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
US-10-820-820-4
sequence of the transcript of human placental RNA Val

```

```

Query Match      100.0%; Score 95; DB 63; Length 95;
Beet Local Similarity 100.0%; Pred. No. 4e-25;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY      1 ACCGUGGUTUCCGUAAGUGUGUGUUNVACAGTUCGCCUACAGCCGAAAGTUCGCCG 60
|||||

```

Db	1	ACCGUGUGUUUCCGUGUGUGUGUGUUUACGUGCGCCUACACGCGAAAGUCCCCGG	60
Dy	61	UUCGAAACCGGCGCGGAAACAAAGACAGUGGCUUUU	95
Dz	61	UUCGAAACCGGCGCGGAAACAAAGACAGUGGCUUUU	95

```

RESULT 5
US-09-623-932-3
Sequence 3, Application US/09623932
GENERAL INFORMATION:
APPLICANT: DIRECTOR-GENERAL OF INDUS. SCIENCE & TECH. AGENCY
APPLICANT: YALISHO PHARMACEUTICAL CO., LTD.
TITLE OF INVENTION: NUCLEIC ACID ENZYME HAVING ALLOSTERIC RNA-CLEAVING
TITLE OF INVENTION: ACTIVITY ON TARGET RNA
FILE REFERENCE: 060764
CURRENT APPLICATION NUMBER: US/09/623,932
CURRENT FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 88
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: The nucleotide
US-09-623-932-3

```

Query Match	78.7%	Score 74.8	DB 28	Length 88
Best Local Similarity	91.9%	Pred. No. 1.8e-17		
Matches 79; Conservative	0	Mismatches 7	Indels 0	Gaps 0

QY 1 ACCGGUGAGUUCAGUAGUGUAGUGUACAGUUGCCUAAACGCGAAAAGUCCCGG 60
Db 1 ACCGGUGAGUUCAGUAGUGUAGUGUACAGUUGCCUAAACGCGAAAAGUCCCGG 60
QY 61 UUCGAAAACGGGCGGAAACAAAGACA 86
Db 61 UUCGAAAACGGGCGACUACAAAACCA 86

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RESULT 6
US-09-623-932A-3
; Sequence 3, Application US/09623932A
; GENERAL INFORMATION:
; APPLICANT: Taiho Pharmaceutical Co., Ltd.
; TITLE OR INVENTION: Nucleic acid enzyme having allosteric RNA-cleaving activity on
; FILE REFERENCE: Q60764
; CURRENT APPLICATION NUMBER: US/09/623,932A
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: JP 60969/1998
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: JP 311098/1998
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: PCT/JP99/01187
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 88
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of tRNAval
US-09-623-932A-3

```

Query Match	78.7%	Score 74.8;	DB 28;	Length 88;
Best Local Similarity	91.9%;	Pred. No. 1.8e-17;		
Matches 79;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0
0y	1	ACCGTUGGCTCCGAGTGAAGGCTGTAATACAGCTCCGCTAAACACGCGAAGGCTCCCG	60	

Db 1 ACCGUTGAGUUCCGUAAGUGAGUGGUUAUACAAGUCCUACACGCGAAAGUCCCCCG 60

QY 61 UUCGAAACCGGAGCGAAACAAAGACA 86

Db 61 UUCGAAACCGGAGCAUACAAAAACCA 86

RESULT 7

```

US-09-974-974-5
: Sequence 5, Application US/09974974
: GENERAL INFORMATION:
: APPLICANT: Kazunari TAIRA
: APPLICANT: Masashi WAKASHINA
: APPLICANT: Tomoko WAKASHINA
: TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
: TITLE OF INVENTION: target RNA by recognizing another molecule
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/09/974, 974
: CURRENT FILING DATE: 2002-03-14
: PRIOR APPLICATION NUMBER: JP 2000-313320
: PRIOR FILING DATE: 2000-10-13
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 88
: TYPE: RNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: tRNAval promoter sequence
: US-09-974-974-5

```

RESULT 8

```

US-10-475-851A-3
: Sequence 3, Application US/10475851A
: GENERAL INFORMATION:
: APPLICANT: TAIWA, Kazunari
: APPLICANT: MARASHINA, Tomoko
: APPLICANT: MARASHINA, Masaki
: APPLICANT: KAWASAKI, Hitoshi
: APPLICANT: HARA, Toshifumi
: APPLICANT: NOZAMA, Iwao
: TITLE OF INVENTION: Novel Nucleic Acid
: FILE REFERENCE: P24426
: CURRENT APPLICATION NUMBER: US/10/475, 851A
: CURRENT FILING DATE: 2003-10-31
: PRIOR APPLICATION NUMBER: PCT/JP02/04322
: PRIOR FILING DATE: 2002-04-30
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 3
: LENGTH: 88
: TYPE: RNA
: ORGANISM: Homo sapiens
: US-10-475-851A-3

```

Page 4

Qy	Db	Qy	Db
1	1	61	61
ACCAGGAGTGTTCGGTAGAGTGAATACAGTGTGCGCCCTAACACGCGAAAAGTCCCGG	ACCGTGGTGTTCGGTAGAGTGAATACAGTGTGCGCCCTAACACGCGAAAAGTCCCGG	TTTCGAAACCGGAGCGGCAAAACAAAGACA	TTTCGAAACCGGAGCGGCAAAACAAAGACA
60	60	86	86

RESULT 9

```

US-10-512-386-1
Sequence 1, Application US/10512386
GENERAL INFORMATION:
APPLICANT: NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY
TITLE OF INVENTION: EXPRESSION SYSTEM FOR STEM-LOOP RNA MOLECULES HAVING RNAI EFFECT
FILE REFERENCE: GPU-A0203Y1P
CURRENT APPLICATION NUMBER: US/10/512.386
PRIOR FILING DATE: 2004-10-25
PRIOR APPLICATION NUMBER: JP 2002-127089
PRIOR FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: JP 2003-4706
PRIOR FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: US 60/449,860
PRIOR FILING DATE: 2003-02-27
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 88
TYPE: RNA
ORGANISM: Homo sapiens
US-10-512-386-1

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RESULT 1

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US-09-718-098-16
; Sequence 16, Application US/09718098
; GENERAL INFORMATION:
; APPLICANT: TANAKA, YAMAMI
; TITLE OF INVENTION: RIBOZYMES TARGETING BRADEION TRANSCRIPTS AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 081356/0155
; CURRENT APPLICATION NUMBER: US/09/718,098
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 91
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: A mutant tRNA(Val)
US-09-718-098-16

```

Qy 61 UUCGAACCGGCGGAAACAAGACA 86
:::|||||
Db 61 TTCGAACCGGCGACTACAAAACCA 86

RESULT 11
US-09-623-932A-20
; Sequence 20, Application US/09623932A
; GENERAL INFORMATION:
; APPLICANT: Taiho Pharmaceutical Co., Ltd.
; APPLICANT: Japan as rep'd by Secretary of Agency of Industrial Science and Technology
; TITLE OF INVENTION: Nucleic acid enzyme having allosteric RNA-cleaving activity on ta
; FILE REFERENCE: 060764
; CURRENT APPLICATION NUMBER: US/09/623,932A
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: JP 60969/1998
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: JP 311098/1998
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: PCT/JP99/01187
; PRIOR FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 128
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Component of tRNAval-Mzr
US-09-623-932A-20

Query Match 78.7%: Score 74.8; DB 28; Length 128;
Best Local Similarity 91.9%; Pred. No. 2e-17; 7; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ACCGUGUGUUCGUGAGUGUAGUGUUAUACAGUUGCGCCUACACGCGAAAGUCCCGG 60
1 ACCGUGUGUUCGUGAGUGUAGUGUUAUACAGUUGCGCCUACACGCGAAAGUCCCGG 60
Db 61 UUCGAACCGGCGGAAACAAGACA 86
61 UUCGAACCGGCGGAAACAAGACA 86

RESULT 12
US-09-623-932A-18
; Sequence 18, Application US/09623932A
; GENERAL INFORMATION:
; APPLICANT: Taiho Pharmaceutical Co., Ltd.
; APPLICANT: Japan as rep'd by Secretary of Agency of Industrial Science and Technology
; TITLE OF INVENTION: Nucleic acid enzyme having allosteric RNA-cleaving activity on ta
; FILE REFERENCE: 060764
; CURRENT APPLICATION NUMBER: US/09/623,932A
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: JP 60969/1998
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: JP 311098/1998
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: PCT/JP99/01187
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 135
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Component of tRNAval-MzL
US-09-623-932A-18

Query Match 78.7%: Score 74.8; DB 28; Length 135;
Best Local Similarity 91.9%; Pred. No. 2e-17;

Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 ACCGUGUGUUCGUGAGUGUAGUGUUAUACAGUUGCGCCUACACGCGAAAGUCCCGG 60
1 ACCGUGUGUUCGUGAGUGUAGUGUUAUACAGUUGCGCCUACACGCGAAAGUCCCGG 60
Db 61 UUCGAACCGGCGGAAACAAGACA 86
61 UUCGAACCGGCGGAAACAAGACA 86

RESULT 13
US-09-984-198A-2
; Sequence 2, Application US/09984198A
; GENERAL INFORMATION:
; APPLICANT: Sano, Masayuki
; APPLICANT: Taiwa, Kazunari
; TITLE OF INVENTION: METHODS FOR SELECTING HIGHLY FUNCTIONAL NUCLEIC ACID MOLECULES
; FILE REFERENCE: 4853.0080-00
; CURRENT APPLICATION NUMBER: US/09/984,198A
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 331347/2000
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 137
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of tRNA-Luc GUA Rz
; NAME/KEY: misc.feature
; LOCATION: (70)-(91)
; OTHER INFORMATION: 22mer random sequence
US-09-984-198A-2

Query Match 78.7%: Score 74.8; DB 45; Length 137;
Best Local Similarity 91.9%; Pred. No. 2e-17; 7; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ACCGUGUGUUCGUGAGUGUAGUGUUAUACAGUUGCGCCUACACGCGAAAGUCCCGG 60
1 ACCGUGUGUUCGUGAGUGUAGUGUUAUACAGUUGCGCCUACACGCGAAAGUCCCGG 60
Db 61 UUCGAACCGGCGGAAACAAGACA 86
61 UUCGAACCGGCGGAAACAAGACA 86

RESULT 14
US-09-974-974-17
; Sequence 17, Application US/09974974
; GENERAL INFORMATION:
; APPLICANT: Kazunari TAIRA
; APPLICANT: Masashi WARASHINA
; APPLICANT: Tomoko WARASHINA
; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
; FILE REFERENCE: target RNA by recognizing another molecule
; CURRENT APPLICATION NUMBER: US/09/974,974
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: JP 2000-313320
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 138
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tRNAval T-MzL

US-09-974-974-17

Query Match	78.7%	Score 74.8;	DB 44;	Length 138;
Best Local Similarity	91.9%;	Pred. No. 2e-17;		
Matches 79; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

QY 1 ACCGUTGGGUTTCGGUAGUGUAGUGUATCACGUTCGGCTTAACACGGGAAAGGUTCCCGG 60

Db 1 ACCGUTGGGUTTCGGUAGUGUAGUGUATCACGUTCGGCTTAACACGGGAAAGGUTCCCGG 60

Qy	61	UUCGAAACCGGGCGGAAACAAGACA	86
Db	61	UUCGAAACCGGGCACTUCAA AAAACCA	86

RESULT 15
US-09-704-525-52

Query March	78.7%	Score 74.8	DB 32,	Length 141;
Best Local	Similarly	91.9%	Pred. No. 2e-17;	
Matches	79; Conservative	0;	Mismatches	7; Indels 0; Gaps 0;

Dy
1 ACCGUGGUTUCCCGAGUGUAAGUGTAAACAGTCGGAAAAGTCCCCCG 60

Dz
1 ACCGUGGUTUCCCGAGUGUAAGUGTAAACAGTCGGAAAAGTCCCCCG 60

Oy	61	UUCGAAACCGGGCGGAAACAAGACA	86
Db	61	UUCGAAACCGGGCAGCAAAAAACCA	86

Search completed: February 18, 2005, 23:15:43
Job time : 2448 secs